

OM protein - protein search, using sw model

Run on: March 17, 2007, 07:24:47 ; Search time 265 Seconds
(without alignments)
16.619 Million cell updates/sec

Title: US-10-527-692-3
Perfect score: 58
Sequence: 1 CYTWNQMNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	58	100.0	9	6	ABB99882	Abb99882 Mouse Wil
2	58	100.0	9	6	ABR44360	Abr44360 Peptide #
3	58	100.0	9	6	ABR38977	Abr38977 Tumour su
4	58	100.0	9	6	ABR44451	Abr44451 WT1 origi
5	58	100.0	9	8	ADN00727	Adn00727 WT1 pepti
6	58	100.0	9	8	ADO43854	Ado43854 Mutant pe
7	58	100.0	9	8	ADQ79628	Adq79628 Human Wil
8	58	100.0	9	9	ADW72808	Adw72808 Human WT1
9	58	100.0	9	9	AEA15681	Aea15681 Human WT1
10	50	86.2	9	3	AAY94203	Aay94203 Human cyt
11	50	86.2	9	3	AAY98534	Aay98534 WT1 deriv
12	50	86.2	9	3	AAY98743	Aay98743 WT1 deriv
13	50	86.2	9	3	AAY80202	Aay80202 Human Wil
14	50	86.2	9	4	AAG61866	Aag61866 Human WT1
15	50	86.2	9	4	AAG62075	Aag62075 Mouse WT1
16	50	86.2	9	4	AAU68633	Aau68633 Human Wil
17	50	86.2	9	4	AAU68842	Aau68842 Mouse Wil
18	50	86.2	9	5	ABG33103	Abg33103 Human WT1
19	50	86.2	9	5	ABG33312	Abg33312 Mouse WT1
20	50	86.2	9	6	ABB99881	Abb99881 Mouse Wil
21	50	86.2	9	6	ABR44359	Abr44359 Peptide #

22	50	86.2	9	6	ABR38975	Abr38975 Tumour su
23	50	86.2	9	6	ABR44450	Abr44450 WT1 origi
24	50	86.2	9	7	ADB67460	Adb67460 Mouse WT1
25	50	86.2	9	7	ADB67251	Adb67251 Human WT1
26	50	86.2	9	7	ADJ80484	Adj80484 Wilm's tu
27	50	86.2	9	7	ADJ80693	Adj80693 Wilm's tu
28	50	86.2	9	8	ADJ83613	Adj83613 Murine WT
29	50	86.2	9	8	ADJ83404	Adj83404 Human WT1
30	50	86.2	9	8	ADL57292	Adl57292 Human WT-
31	50	86.2	9	8	ADL57501	Adl57501 Mouse WT-
32	50	86.2	9	8	ADN00726	Adn00726 WT1 pepti
33	50	86.2	9	8	ADO08847	Ado08847 Human WT1
34	50	86.2	9	8	ADO09056	Ado09056 Mouse WT1
35	50	86.2	9	8	ADO43853	Ado43853 Peptide d
36	50	86.2	9	8	ADQ79595	Adq79595 Human Wil
37	50	86.2	9	9	ADW72807	Adw72807 Human WT1
38	50	86.2	9	9	AEA15680	Aea15680 Human WT1
39	50	86.2	9	9	AEA23127	Aea23127 Human Wil
40	50	86.2	9	10	AEH16052	Aeh16052 Human Wil
41	50	86.2	9	10	AEJ93742	Aej93742 Human WT1
42	50	86.2	9	10	AEK11111	Aek11111 Autoantib
43	50	86.2	9	10	AEK62610	Aek62610 Exemplary
44	50	86.2	9	10	AEL42685	Ael42685 Human Wil
45	50	86.2	15	8	ADL57751	Adl57751 Human Wil

ALIGNMENTS

RESULT 1

ABB99882

ID ABB99882 standard; peptide; 9 AA.

XX

AC ABB99882;

XX

DT 27-JAN-2003 (first entry)

XX

DE Mouse Wilm's tumour antigen WT1 modified peptide core sequence.

XX

KW Mouse; murine; Wilm's tumour antigen; WT1; modified WT1 peptide; vaccine;
KW immunotherapy; cancer; leukaemia; solid tumour; mutant; mutein.

XX

OS Mus sp.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 2

FT /note= "Tyr replaces wild-type Met"

XX

PN WO200279253-A1.

XX

PD 10-OCT-2002.

XX

PF 22-MAR-2002; 2002WO-JP002794.

XX

PR 22-MAR-2001; 2001JP-00083250.

XX

PA (SUGI/) SUGIYAMA H.

XX

PI Sugiyama H;

XX

DR WPI; 2003-046799/04.

XX

PT Cancer antigen WT1 modified peptides and DNA encoding them for cancer
PT immunotherapy.

XX

PS Claim 1; Page 16; 30pp; Japanese.

XX

CC The invention relates to modified peptides derived from the murine Wilm's
CC tumour antigen WT1 (ABB99880). The peptides of the invention are 9-30
CC amino acids long and comprise the sequence Cys-Tyr-Thr-Trp-Asn-Gln-Met-

CC Asn-Leu (ABB99882). Cancer vaccines comprising modified WT1 peptides of
 CC the invention or DNA encoding them, and antigen presenting cells
 CC (including cytotoxic T-cells) which present a peptide of the invention
 CC complexed with a major histocompatibility complex (MHC) class I molecule,
 CC can be used in the immunotherapy of leukaemia and solid tumours such as
 CC cancers of the bladder, colon, breast, ovary, liver, skin, stomach,
 CC prostate, testis, lung and uterus. The present sequence represents the
 CC modified murine WT1 peptide core sequence, which is specifically claimed

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.3e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 |||||
 Db 1 CYTWNQMNL 9

RESULT 2

ABR44360

ID ABR44360 standard; peptide; 9 AA.

XX

AC ABR44360;

XX

DT 14-JUL-2003 (first entry)

XX

DE Peptide #3 related to the induction of antigen-specific T cells.

XX

KW Antigen-specific T cells; cytostatic; cancer.

XX

OS Synthetic.

XX

PN WO2003028758-A1.

XX

PD 10-APR-2003.

XX

PF 27-SEP-2002; 2002WO-JP009997.

XX

PR 28-SEP-2001; 2001JP-00301224.

XX

PA (SUGI/) SUGIYAMA H.

XX

PA (AZUM/) AZUMA I.

XX

PI Sugiyama H, Azuma I;

XX

DR WPI; 2003-354695/33.

XX

PT Inducing antigen-specific T cells in patients by administering
 PT compositions containing antigen protein or peptide and bovine tubercle
 PT bacillus BCG-strain cell wall skeleton, in treating cancer.

XX

PS Claim 8; Page 29; 50pp; Japanese.

XX

CC The present invention relates to inducing antigen-specific T cells by to
 CC a patient, which is cytostatic in its action. The method and drug
 CC compositions are applicable in preventing or treating cancer which is
 CC considered convenient and efficient. The present sequence represents a
 CC peptide related to the method for inducing antigen-specific T cells

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.3e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 |||||
 Db 1 CYTWNQMNL 9

RESULT 3

ABR38977

ID ABR38977 standard; peptide; 9 AA.

XX

AC ABR38977;

XX

DT 27-JUN-2003 (first entry)

XX

DE Tumour suppressor gene WT1 peptide fragment #SEQ ID 9.

XX

KW Tumour supressor; WT1; cytostatic; vaccine; cancer; leukaemia;
KW myelosis syndrome; malignant lymphoma; multiple myeloma; stomach; colon;
KW lung; breast; embryonic carcinoma; liver; skin; bladder; prostate;
KW metrocacinoma; cervical; ovarian.

XX

OS Synthetic.

XX

PN WO2003002142-A1.

XX

PD 09-JAN-2003.

XX

PF 28-JUN-2002; 2002WO-JP006597.

XX

PR 29-JUN-2001; 2001JP-00199449.

XX

PA (CHUS) CHUGAI SEIYAKU KK.

PA (MAYU/) MAYUMI T.

PA (SUGI/) SUGIYAMA H.

XX

PI Mayumi T, Sugiyama H, Ohsugi Y;

XX

DR WPI; 2003-201466/19.

XX

PT Cancer vaccines containing cancer antigen based on tumor suppressor gene
PT WT1 product and cationic liposomes, applicable in therapy of e.g.
PT leukemia, malignant lymphoma, stomach cancer and ovarian cancer.

XX

PS Claim 7; Page 7; 31pp; Japanese.

XX

CC The invention relates to cancer vaccines, comprising a tumour antigen and
CC cationic liposomes with a tumour suppressor gene WT1 product or its
CC peptide or modified material as the active ingredient. The vaccines are
CC applicable in therapy of cancer e.g. leukaemia, myelosis syndrome,
CC malignant lymphoma, multiple myeloma, stomach cancer, colon cancer, lung
CC cancer, breast cancer, embryonic carcinoma, liver cancer, skin cancer,
CC bladder cancer, prostate cancer, metrocacinoma, cervical cancer or
CC ovarian cancer..The current sequence represents a tumour suppressor gene
CC WT1 peptide fragment of the invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

|||||||

Db 1 CYTWNQMNL 9

RESULT 4

ABR44451

ID ABR44451 standard; peptide; 9 AA.

XX

AC ABR44451;

XX

DT 25-JUL-2003 (first entry)

XX

DE WT1 originated cancer antigen peptide #SEQ ID 4.

XX

KW Immunopotentiators; wilms tumour protein; WT; cytostatic; virucide;
 KW cancer; viral infection.
 XX
 OS Synthetic.
 XX
 PN WO2003028757-A1.
 XX
 PD 10-APR-2003.
 XX
 PF 27-SEP-2002; 2002WO-JP009993.
 XX
 PR 28-SEP-2001; 2001JP-00301206.
 XX
 PA (SUGI/) SUGIYAMA H.
 XX
 PI Sugiyama H;
 XX
 DR WPI; 2003-354694/33.
 XX
 PT Inducing antigen-specific T cells in patients by administering
 PT compositions containing antigen protein or peptide and non-specific
 PT immunopotentiator, in preventing or treating cancer.
 XX
 PS Claim 7; Page 37; 59pp; Japanese.
 XX
 CC The invention relates to inducing antigen-specific T cells by giving to a
 CC patient compositions containing (a) an antigen protein or peptide as the
 CC active ingredient, and a composition (b) containing a non-specific
 CC immunopotentiator, where (b) is administered before (a). The method and
 CC drug compositions of the invention are useful for preventing or treating
 CC cancer, and also viral infections. The current sequence represents a WT1
 CC originated cancer antigen peptide of the invention
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.3e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 |||||
 Db 1 CYTWNQMNL 9

RESULT 5
 ADN00727

ID ADN00727 standard; protein; 9 AA.
 XX
 AC ADN00727;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE WT1 peptide, SEQ ID 3.
 XX
 KW Cytostatic; WT1; cancer; antigen; myeloma; skin cancer; liver cancer;
 KW lung cancer; prostate cancer; ovarian cancer.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2004024175-A1.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-JP011675.
 XX
 PR 12-SEP-2002; 2002JP-00266876.
 XX
 PA (SUGI/) SUGIYAMA H.
 XX
 PI Sugiyama H;

XX
DR WPI; 2004-269896/25.
XX
PT Cancer-antigen peptide preparations containing WT1-originated HLA-A24-
PT restricted peptide with CTL induction activity, e.g. water-in-oil type
PT emulsion as vaccine for myeloma, skin cancer, liver cancer and lung
PT cancer.
XX
PS Claim 1; SEQ ID NO 3; 24pp; Japanese.
XX
CC The present invention relates to a water-in-oil type emulsion containing
CC WT1-origin cancer antigen peptides (ADN00726 and/or ADN00727) as the
CC active ingredient. The emulsion has CTL induction activity and is
CC applicable as a cancer vaccine for myeloma, skin cancer, liver cancer,
CC lung cancer, prostate cancer, ovarian cancer etc.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 1 CYTWNQMNL 9

RESULT 6
ADO43854
ID ADO43854 standard; peptide; 9 AA.
XX
AC ADO43854;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mutant peptide based on human WT1 polypeptide residues 235-243.
XX
KW Human; WT1; CTL induction; cancer vaccine; stomach cancer;
KW prostate cancer; ovarian cancer.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004026897-A1.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-JP011974.
XX
PR 20-SEP-2002; 2002JP-00275264.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (SUGI/) SUGIYAMA H.
XX
PI Sugiyama H, Gotoh M, Takasu H, Samizo F, Kusunose N, Nakatsuka M;
XX
DR WPI; 2004-295379/27.
XX
PT Novel WT1 substitution peptides with cysteine replaced by specific amino
PT acid residue and their encoded polynucleotide for cancer vaccines with
PT CTL induction activity for treatment of e.g. stomach cancer and prostate
PT cancer.
XX
PS Example 1; Page 31; 65pp; Japanese.
XX
CC The specification describes WT1 substitution peptides, in which a
CC cysteine residue is substituted with another amino acid residue. The WT1
CC substitution peptides have CTL induction activity. Peptides of the
CC invention are used in cancer vaccines, which are applicable in the
CC treatment of e.g. stomach cancer, prostate cancer and ovarian cancer. The

CC present sequence represents a peptide derived from human WT1 residues 235
CC -243, where residue 236 is changed from methionine to tyrosine.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

|||||||

Db 1 CYTWNQMNL 9

RESULT 7

ADQ79628

ID ADQ79628 standard; peptide; 9 AA.

XX

AC ADQ79628;

XX

DT 21-OCT-2004 (first entry)

XX

DE Human Wilms Tumour 1, WT1, related peptide SEQ ID 44.

XX

KW Cytostatic; Anticancer; vaccine; cancer antigen; cancer; WT1;

KW Wilms Tumour 1.

XX

OS Synthetic.

XX

PN WO2004063217-A1.

XX

PD 29-JUL-2004.

XX

PF 15-JAN-2004; 2004WO-JP000254.

XX

PR 15-JAN-2003; 2003JP-00007122.

XX

PA (SUGI/) SUGIYAMA H.

PA (CHUS) CHUGAI SEIYAKU KK.

PA (SUMU) SUMITOMO PHARM CO LTD.

XX

PI Takasu H, Samizo F;

XX

DR WPI; 2004-561874/54.

XX

PT New cancer antigen useful as a cytotoxic T cell inducing anti-cancer

PT vaccine comprises a dimer of disulfide-linked peptide monomers.

XX

PS Claim 6; SEQ ID NO 44; 61pp; Japanese.

XX

CC The present invention relates to novel cancer antigens comprised of
CC dimerised peptides which have cytotoxic T-lymphocyte inducing activity.

CC The dimerised peptides comprise two disulfide-linked monomers of 7-30

CC amino acid residues, each having at least one cysteine residue. Also

CC claimed is a pharmaceutical composition, comprising the cancer antigen

CC and a carrier. The cancer antigens are useful for manufacturing cancer

CC vaccine, and for treating or preventing cancer, in the patient with WT1

CC positivity, such as leukaemia, malignant lymphoma, myelodysplastic

CC syndrome, cancer of breast, stomach, colon, lung, embryonic cell, skin,

CC bladder, prostatic, uterine cervix, uterine, ovarian, hepatic carcinoma.

CC The peptide monomers (ADQ79586-ADQ79656) are derived from the human Wilms

CC Tumour 1 protein, WT1 (ADQ79585).

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

|||||||

Db 1 CYTWNQMNL 9

RESULT 8

ADW72808

ID ADW72808 standard; peptide; 9 AA.

XX

AC ADW72808;

XX

DT 24-MAR-2005 (first entry)

XX

DE Human WT1-associated protein fragment SEQ ID NO 3.

XX

KW WT1 protein; Wilm's tumor gene 1; vaccine; cytotoxic T cell;

KW cancer antigen peptide; HLA-A2U antigen; HLA-A2 antigen; diagnosis.

XX

OS Homo sapiens.

XX

PN WO2005001117-A1.

XX

PD 06-JAN-2005.

XX

PF 25-JUN-2004; 2004WO-JP009378.

XX

PR 27-JUN-2003; 2003JP-00184436.

PR 12-MAR-2004; 2004JP-00070497.

XX

PA (SUGI/) SUGIYAMA H.

XX

PI Sugiyama H;

XX

DR WPI; 2005-101267/11.

XX

PT Selecting patient with high Wilm's tumor gene 1 (WT1) vaccine

PT responsiveness, by measuring frequency of WT1 specific CTL progenitor

PT cell in healthy and test subject, selecting patient if frequency is

PT higher than healthy subject.

XX

PS Claim 7; SEQ ID NO 3; 65pp; Japanese.

XX

CC This invention describes novel methods of selecting a patient with high
CC Wilm's tumor gene 1 (WT1) vaccine responsiveness by isolating biological
CC sample containing cytotoxic T cell (CTL) progenitor cells from the
CC patient, measuring existence frequency or quantity of WT1 specific CTL
CC progenitor cell and comparing values with healthy subject, and
CC determining or judging WT1 vaccine responsiveness if the measured
CC frequency or quantity of WT1 is higher than healthy subject. The method
CC involves contacting a patient sample containing CTL progenitor cells with
CC a HLA tetramer containing the cancer antigen peptide derived from WT1,
CC anti-CDR antibody, anti-CD45RA antibody and anti-CD27 antibody and
CC measuring the ratio of CD8-positive or CD8/CD3 positive and CD45RA
CC positive, and CD27-negative in effector type CTL progenitor cell then
CC determining whether the measured value is higher than in healthy subject,
CC and judging WT1 vaccine responsiveness. The HLA antigen which is the
CC structural component of HLA monomer, HLA dimer, HLA tetramer, HLA
CC pentamer, described in the invention is HLA-A2U antigen or HLA-A2
CC antigen. This sequence represents a fragment of the human WT1-associated
CC protein.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.3e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

|||||||

Db 1 CYTWNQMNL 9

RESULT 9

AEA15681
ID AEA15681 standard; peptide; 9 AA.
XX
AC AEA15681;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human WT1-derived HLA-DRB1*0405 antigen-related peptide SeqID28.
XX
KW cancer; vaccine; cytostatic; T-cell.
XX
OS Unidentified.
XX
PN WO2005045027-A1.
XX
PD 19-MAY-2005.
XX
PF 04-NOV-2004; 2004WO-JP016336.
XX
PR 05-NOV-2003; 2003JP-00375603.
XX
PA (SUGI/) SUGIYAMA H.
XX
PI Sugiyama H;
XX
DR WPI; 2005-366845/37.
XX
PT New peptide capable of binding to WT1 derived HLA-DRB1*0405
PT antigen, useful for preventing or treating cancer, and enhancing a cancer
PT vaccine.
XX
PS Disclosure; SEQ ID NO 28; 72pp; Japanese.
XX
CC This invention relates to a novel peptide capable of binding to WT1-
CC derived HLA-DRB1*0405 antigen, and comprising 10-25 contiguous amino
CC acids of a (SEQ ID No:1) sequence, given in specification. The invention
CC may be useful for the development of compounds with a cytostatic activity
CC acting as a helper T cell inducer or cancer vaccine enhancer. The
CC invention may be useful in the manufacture of a therapeutic or
CC prophylactic agent of cancer or as an enhancer of a cancer vaccine. The
CC invention enables cancer to be treated efficiently. The present sequence
CC is that of a peptide of the invention which is related to the invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 58; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | | |
Db 1 CYTWNQMNL 9

RESULT 10
AA94203
ID AA94203 standard; peptide; 9 AA.
XX
AC AA94203;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human cytotoxic T lymphocyte-recognised WT1 peptide WT235-43.
XX
KW WT235-43; peptide; epitope; Wilm's tumour gene; leukaemia; breast cancer;
KW melanoma; ovarian cancer; immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200026249-A1.
XX

PD 11-MAY-2000.
 XX
 PF 02-NOV-1999; 99WO-GB003572.
 XX
 PR 02-NOV-1998; 98GB-00023897.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Stauss HJ, Gao L;
 XX
 DR WPI; 2000-376123/32.
 XX
 PT Novel peptides comprising WT-1 and GATA-1 epitopes, their fragments or
 PT variants, useful as vaccines for cancer immunotherapy.
 XX
 PS Claim 2; Page 74; 93pp; English.
 XX
 CC The present sequence is peptide epitope WT235-43, produced by WT1
 CC expressing cells and found at residues 235-243 of the WT1 protein, which
 CC is recognised by cytotoxic T lymphocytes. WT1 is aberrantly expressed in
 CC leukaemias, breast cancer, melanoma and ovarian cancer. The peptide can
 CC be used as a vaccine to stimulate the elimination, by cytotoxic T
 CC lymphocytes, of cancer cells aberrantly expressing WT1. In addition, the
 CC nucleic acid encoding the peptide may also be used in the same manner.
 CC Alternatively, the peptide may be used in vitro to produce activated
 CC cytotoxic T lymphocytes
 XX
 SQ Sequence 9 AA;

Query Match 86.2%; Score 50; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.3e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9.
 | | | | | | | |
 Db 1 CMTWNQMNL 9

RESULT 11

AAY98534
 ID AAY98534 standard; peptide; 9 AA.
 XX
 AC AAY98534;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE WT1 derived immunogenic peptide SEQ ID NO:49.
 XX
 KW WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;
 KW metastatic disease; mouse; human; Wilm's tumour; immune response;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200018795-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 30-SEP-1999; 99WO-US022819.
 XX
 PR 30-SEP-1998; 98US-00164223.
 PR 25-MAR-1999; 99US-00276484.
 XX
 PA (CORI-) CORIXA CORP.
 PA (GAIG/) GAIGER A.
 XX
 PI Gaiger A, Cheever M;
 XX
 DR WPI; 2000-293107/25.
 XX
 PT Novel polypeptides comprising an immunogenic portion of a native WT1

PT polypeptide, useful for inhibiting the development of malignant diseases
PT associated with WT1 expression e.g. leukemia or cancer.

XX

PS Claim 4; Page 151; 193pp; English.

XX

CC The present invention describes polypeptides (I) comprising an
CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
CC WT1, (or variants of the immunogenic portion retaining the ability to
CC react with WT1-specific antisera and/or T-cell lines or clones) and
CC comprising 16 consecutive amino acids (aa) or less of a native WT1
CC polypeptide. The polypeptides are useful therapeutically and to
CC manufacture medicaments for enhancing/inducing an immune response in
CC patients. The polypeptides, mimetics or polynucleotides can be included
CC with a carrier/excipient in pharmaceutical compositions or with a non-
CC specific immune response enhancer (e.g. an adjuvant or enhancer
CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
CC compositions and vaccines can be administered to human patients to
CC enhance or induce an immune response specific for WT1 or a cell
CC expressing WT1, useful to inhibit the development of malignant diseases
CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
CC AAY98501 to AAY98811 represent polypeptide sequences, and AAA13848 to
CC AAA13862 represent PCR primers, used in the exemplification of the
CC present invention

XX

SQ Sequence 9 AA;

Query Match 86.2%; Score 50; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 2.3e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

| | | | | | | |

Db 1 CMTWNQMNL 9

RESULT 12

AAAY98743

ID AAY98743 standard; peptide; 9 AA.

XX

AC AAY98743;

XX

DT 31-JUL-2000 (first entry)

XX

DE WT1 derived immunogenic peptide SEQ ID NO:258.

XX

KW WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia;

KW metastatic disease; mouse; human; Wilm's tumour; immune response;

KW vaccine.

XX

OS Mus musculus.

XX

PN WO200018795-A2.

XX

PD 06-APR-2000.

XX

PF 30-SEP-1999; 99WO-US022819.

XX

PR 30-SEP-1998; 98US-00164223.

PR 25-MAR-1999; 99US-00276484.

XX

PA (CORI-) CORIXA CORP.

PA (GAIG/) GAIGER A.

XX

PI Gaiger A, Cheever M;

XX

DR WPI; 2000-293107/25.

XX

PT Novel polypeptides comprising an immunogenic portion of a native WT1
PT polypeptide, useful for inhibiting the development of malignant diseases

PT associated with WT1 expression e.g. leukemia or cancer.
 XX
 PS Claim 4; Page 181; 193pp; English.
 XX
 CC The present invention describes polypeptides (I) comprising an
 CC immunogenic portion of a native Wilm's Tumour gene product polypeptide,
 CC WT1, (or variants of the immunogenic portion retaining the ability to
 CC react with WT1-specific antisera and/or T-cell lines or clones) and
 CC comprising 16 consecutive amino acids (aa) or less of a native WT1
 CC polypeptide. The polypeptides are useful therapeutically and to
 CC manufacture medicaments for enhancing/inducing an immune response in
 CC patients. The polypeptides, mimetics or polynucleotides can be included
 CC with a carrier/excipient in pharmaceutical compositions or with a non-
 CC specific immune response enhancer (e.g. an adjuvant or enhancer
 CC preferentially enhancing a T cell response) in vaccines. Pharmaceutical
 CC compositions and vaccines can be administered to human patients to
 CC enhance or induce an immune response specific for WT1 or a cell
 CC expressing WT1, useful to inhibit the development of malignant diseases
 CC associated with WT1 expression, e.g. leukemia (especially acute/chronic
 CC myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
 CC breast, lung, thyroid or gastrointestinal cancer, or a melanoma).
 CC AAY98501 to AAY98811 represent polypeptide sequences, and AAA13848 to
 CC AAA13862 represent PCR primers, used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 9 AA;

Query Match 86.2%; Score 50; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.3e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 1 CMTWNQMNL 9

RESULT 13
 AAY80202
 ID AAY80202 standard; peptide; 9 AA.
 XX
 AC AAY80202;
 XX
 DT 24-MAY-2000 (first entry)
 XX
 DE Human Wilms' tumour suppressor gene WT1 product peptide SEQ ID NO:7.
 XX
 KW Wilm's tumour suppressor gene; WT1; cancer; antigen; vaccine; MHC;
 KW major histocompatibility complex; leukaemia; tumour; antitumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200006602-A1.
 XX
 PD 10-FEB-2000.
 XX
 PF 30-JUL-1999; 99WO-JP004130.
 XX
 PR 31-JUL-1998; 98JP-00218093.
 XX
 PA (SUGI/) SUGIYAMA H.
 XX
 PI Sugiyama H, Oka Y;
 XX
 DR WPI; 2000-195264/17.
 XX
 PT Cancer antigens based on Wilm's tumor suppressor gene WT1 product or
 PT peptide derivatives, for cancer vaccines in treating leukemia and solid
 PT tumors e.g. stomach cancer, skin cancer, lung cancer and breast cancer.
 XX
 PS Claim 5; Page 18; 48pp; Japanese.
 XX

CC The present invention describes a cancer antigen containing the active
 CC component of Wilms' tumour suppressor gene WT1 product, or partial
 CC peptides, for cancer vaccines in treating leukaemia and solid tumours.
 CC The cancer antigens are useful for cancer vaccines in treating leukaemia,
 CC bone-marrow abnormal formation syndrome, malignant lymphoma, multiple
 CC myeloma, stomach cancer, cancer of the large intestine, lung cancer,
 CC breast cancer, blastoma, liver cancer, skin cancer, bladder cancer,
 CC prostate cancer, uterus cancer, cervical cancer, or ovary cancer. The
 CC present sequence represents a peptide from the human Wilms' tumour
 CC suppressor gene WT1 product

XX

SQ Sequence 9 AA;

Query Match 86.2%; Score 50; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.3e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | | | | | | |
 Db 1 CMTWNQMNL 9

RESULT 14

AAG61866

ID AAG61866 standard; peptide; 9 AA.

XX

AC AAG61866;

XX

DT 06-JUL-2001 (first entry)

XX

DE Human WT1 immunogenic peptide SEQ ID NO: 49.

XX

KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;
 KW chromosome 11p13; zinc finger transcription factor.

XX

OS Homo sapiens.

XX

PN WO200125273-A2.

XX

PD 12-APR-2001.

XX

PF 04-OCT-2000; 2000WO-US027465.

XX

PR 04-OCT-1999; 99US-0157459P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Skeiky YAW, Xu J, Cheever MA, Reed SG;

XX

DR WPI; 2001-328324/34.

XX

PT Polypeptide comprising part of the Wilms Tumor gene product sequence is
 PT used in the diagnosis and treatment of malignant diseases e.g. leukemia
 PT and cancer associated with WTI.

XX

PS Claim 4; Page 162; 228pp; English.

XX

CC The present invention describes compositions comprising peptides derived
 CC from the Wilm's tumour protein WT1 and methods for their use in treating
 CC malignant diseases. Peptides derived from both the murine and human WT1
 CC proteins are provided. The human WT1 gene is found on chromosome 11p13,
 CC and the protein was shown to be a zinc finger transcription factor. The
 CC immunogenic peptides of the invention are particularly useful in the
 CC diagnosis and treatment of cancer and leukaemia. The present sequence is
 CC a polypeptide described in the exemplification of the invention

XX

SQ Sequence 9 AA;

Query Match 86.2%; Score 50; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.3e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 1 CMTWNQMNL 9

RESULT 15

AAG62075

ID AAG62075 standard; peptide; 9 AA.

XX

AC AAG62075;

XX

DT 06-JUL-2001 (first entry)

XX

DE Mouse WT1 immunogenic peptide SEQ ID NO: 258.

XX

KW Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour gene;

KW chromosome 11p13; zinc finger transcription factor.

XX

OS Mus musculus.

XX

PN WO200125273-A2.

XX

PD 12-APR-2001.

XX

PF 04-OCT-2000; 2000WO-US027465.

XX

PR 04-OCT-1999; 99US-0157459P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Skeiky YAW, Xu J, Cheever MA, Reed SG;

XX

DR WPI; 2001-328324/34.

XX

PT Polypeptide comprising part of the Wilms Tumor gene product sequence is

PT used in the diagnosis and treatment of malignant diseases e.g. leukemia

PT and cancer associated with WT1.

XX

PS Claim 4; Page 195; 228pp; English.

XX

CC The present invention describes compositions comprising peptides derived

CC from the Wilm's tumour protein WT1 and methods for their use in treating

CC malignant diseases. Peptides derived from both the murine and human WT1

CC proteins are provided. The human WT1 gene is found on chromosome 11p13,

CC and the protein was shown to be a zinc finger transcription factor. The

CC immunogenic peptides of the invention are particularly useful in the

CC diagnosis and treatment of cancer and leukaemia. The present sequence is

CC a polypeptide described in the exemplification of the invention

XX

SQ Sequence 9 AA;

Query Match 86.2%; Score 50; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 2.3e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

| | | | |

Db 1 CMTWNQMNL 9

Search completed: March 17, 2007, 07:29:14

Job time : 267 secs

Sugiyama 10527692 PIR search

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2007, 07:35:31 ; Search time 31 Seconds
(without alignments)
27.934 Million cell updates/sec

Title: US-10-527-692-3
Perfect score: 58
Sequence: 1 CYTWNQMNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues.

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	86.2	410	2	JC5046	Wilms' tumor suppr
2	50	86.2	448	2	S33926	Wilms' tumor prote
3	50	86.2	449	2	A38080	Wilms tumor suscep
4	50	86.2	449	2	A39692	Wilms' tumor prote
5	39	67.2	527	2	G89999	conserved hypothet
6	38	65.5	498	2	S68588	nicotinic acetylch
7	37	63.8	347	2	AE0716	hypothetical prote
8	37	63.8	422	2	S63226	hypothetical prote
9	36	62.1	310	2	G83933	dipeptidase BH2271
10	36	62.1	1579	2	S59801	protein kinase SSK
11	35	60.3	143	2	S50549	hypothetical prote
12	35	60.3	314	2	T39922	pop3, a WD repeat
13	35	60.3	338	2	T23351	hypothetical prote
14	35	60.3	530	2	JC7979	cellobiohydrolase
15	35	60.3	615	2	T20187	hypothetical prote
16	35	60.3	712	2	S19387	saccharolysin (EC
17	35	60.3	2322	2	T10542	hypothetical prote
18	35	60.3	2406	2	A54148	odz protein - frui
19	35	60.3	2515	2	S47008	tenascin-like prot
20	34	58.6	116	2	S73442	hypothetical prote
21	34	58.6	183	2	T51405	ribosomal protein
22	34	58.6	202	2	D86776	amidotransferase (
23	34	58.6	202	2	I45734	imidazoleglycerol-
24	34	58.6	233	2	H87583	hypothetical prote
25	34	58.6	245	2	S56827	conserved hypothet

26	34	58.6	268	2	AG2594	enoyl-(acyl-carrie
27	34	58.6	270	2	H97376	enoyl-(acyl-carrie
28	34	58.6	279	2	JC2106	rolB protein - Agr
29	34	58.6	279	2	S52639	hypothetical prote
30	34	58.6	319	2	A97103	hypothetical prote
31	34	58.6	371	2	T00438	probable MYB famil
32	34	58.6	371	2	T51636	myb-related transc
33	34	58.6	372	2	B81952	probable type II r
34	34	58.6	385	2	S64340	hypothetical prote
35	34	58.6	447	2	H86534	hypothetical prote
36	34	58.6	447	2	H72089	hypothetical prote
37	34	58.6	463	2	D64579	glutamate-tRNA lig
38	34	58.6	463	2	D71932	glutamate-tRNA lig
39	34	58.6	463	2	B81580	hypothetical prote
40	34	58.6	481	2	S76820	hypothetical prote
41	34	58.6	495	2	D71307	conserved hypothet
42	34	58.6	524	2	T20872	hypothetical prote
43	34	58.6	528	2	D86456	probable protein k
44	34	58.6	529	2	G72605	probable acid-CoA
45	34	58.6	534	2	T27054	hypothetical prote

ALIGNMENTS

RESULT 1

JC5046

Wilms' tumor suppressor protein - African clawed frog

N;Alternate names: WT1

C;Species: *Xenopus laevis* (African clawed frog)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004

C;Accession: JC5046

R;Semba, K.; Saito-Ueno, R.; Takayama, G.; Kondo, M.

Gene 175, 167-172, 1996

A;Title: cDNA cloning and its pronephros-specific expression of the Wilms' tumor suppressor gene, WT1, from *Xenopus laevis*.

A;Reference number: JC5046; MUID:97074667; PMID:8917094

A;Contents: testis

A;Accession: JC5046

A;Molecule type: mRNA

A;Residues: 1-410 <SEM>

A;Cross-references: UNIPROT:P79958; UNIPARC:UPI000017BFA3; DDBJ:D82051

C;Comment: This protein is involved in kidney morphogenesis.

C;Genetics:

A;Gene: wt1

Query Match 86.2%; Score 50; DB 2; Length 410;
 Best Local Similarity 88.9%; Pred. No. 0.63;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | | | | | | |
 Db 212 CMTWNQMNL 220

RESULT 2

S33926

Wilms' tumor protein WT1 - rat

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-May-1996

C;Accession: S33926

R;Sharma, P.M.; Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.

Cancer Res. 52, 6407-6412, 1992

A;Title: Molecular cloning of rat Wilms' tumor complementary DNA and a study of messenger RNA expression in the urogenital system and the brain.

A;Reference number: S33926; MUID:93046155; PMID:1330293

A;Accession: S33926

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-448 <SHA>

A;Cross-references: UNIPARC:UPI000017CA1C; EMBL:X69716

C;Genetics:
A;Gene: WT1
C;Keywords: tumor suppressor

Query Match 86.2%; Score 50; DB 2; Length 448;
Best Local Similarity 88.9%; Pred. No. 0.69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 234 CMTWNQMNL 242

RESULT 3

A38080

Wilms tumor susceptibility protein WT1 - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000

C;Accession: A38080; S08273; A34673; I38504; I52811; I58315; A56411; S26286

R;Gessler, M.; Konig, A.; Bruns, G.A.

Genomics 12, 807-813, 1992

A;Title: The genomic organization and expression of the WT1 gene.

A;Reference number: A38080; MUID:92241883; PMID:1572653

A;Accession: A38080

A;Molecule type: DNA

A;Residues: 1-449 <GES1>

A;Cross-references: UNIPARC:UPI000017C420; GB:X61631; GB:S99414; NID:g37981;

PIDN:CAA43819.1; PID:g825731

A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated upstream to the sequenced region

A;Note: sequence extracted from NCBI backbone (NCBIN:99414, NCBIN:99422, NCBIN:99479, NCBIN:99543, NCBIN:99546, NCBIN:99553, NCBIN:99558, NCBIN:99567)

A;Note: the sequence in GenBank entry HSWTGEE1, release 113.0, PIDN:CAA43819.1 differs by omitting residues 408-410, an alternate splice form

R;Gessler, M.; Poustka, A.; Cavenee, W.; Neve, R.L.; Orkin, S.H.; Bruns, G.A.P.

Nature 343, 774-778, 1990

A;Title: Homozygous deletion in Wilms tumours of a zinc-finger gene identified by chromosome jumping.

A;Reference number: S08273; MUID:90158822; PMID:2154702

A;Accession: S08273

A;Molecule type: mRNA

A;Residues:

'SRQRPHPGALRNPTACPLPHFPSPSLPPTHSPTHPRAGTAAQAPGPRRLAAILDFLLLQDPASTCVPEPASQHTLRSGPGCLQQPEQ QGVRDPGGIWAKLGAEEASERLQGRSRGASGSEPQQ',1-386,'T',388-449 <GES2>

A;Cross-references: UNIPARC:UPI000016B316; EMBL:X51630; NID:g37977; PIDN:CAA35956.1; PID:g37978

R;Call, K.M.; Glaser, T.; Ito, C.Y.; Buckler, A.J.; Pelletier, J.; Haber, D.A.; Rose, E.A.; Kral, A.; Yeger, H.; Lewis, W.H.; Jones, C.; Housman, D.E.

Cell 60, 509-520, 1990

A;Title: Isolation and characterization of a zinc finger polypeptide gene at the human chromosome 11 Wilms' tumor locus.

A;Reference number: A34673; MUID:90150277; PMID:2154335

A;Accession: A34673

A;Molecule type: mRNA

A;Residues: 85-249,267-364,'F',366-386,'T',388-407,411-449 <CAL>

A;Cross-references: UNIPARC:UPI0000147983; GB:M30393; NID:g340381; PIDN:AAA36810.1; PID:g340382

R;Haber, D.A.; Sohn, R.L.; Buckler, A.J.; Pelletier, J.; Call, K.M.; Housman, D.E. Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991

A;Title: Alternative splicing and genomic structure of the Wilms tumor gene WT1.

A;Reference number: A56411; MUID:92052142; PMID:1658787

A;Contents: annotation; alternative splicing

R;Phelan, S.A.; Lindberg, C.; Call, K.M.

Cell Growth Differ. 5, 677-686, 1994

A;Title: Wilms' tumor gene, WT1, mRNA is down-regulated during induction of erythroid and megakaryocytic differentiation of K562 cells.

A;Reference number: I38504; MUID:94368704; PMID:8086342

A;Accession: I38504

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-18 <PHE>

A;Cross-references: UNIPARC:UPI000000052B; EMBL:U06486; NID:g473563; PIDN:AAA62865.1; PID:g458432
R;Pelletier, J.; Bruening, W.; Kashtan, C.E.; Mauer, S.M.; Manivel, J.C.; Striegel, J.E.; Houghton, D.C.; Junien, C.; Habib, R.; Fouser, L.
Cell 67, 437-447, 1991
A;Title: Germline mutations in the Wilms' tumor suppressor gene are associated with abnormal urogenital development in Denys-Drash syndrome.
A;Reference number: I52811; MUID:92005721; PMID:1655284
A;Accession: I52811
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 355-365,'H',367-377 <PEL>
A;Cross-references: UNIPARC:UPI000011DDFA; GB:S61513; NID:g237599; PIDN:AAB20109.1; PID:g237600
A;Note: mutant form
R;Hamilton, T.B.; Barilla, K.C.; Romaniuk, P.J.
Nucleic Acids Res. 23, 277-284, 1995
A;Title: High affinity binding sites for the Wilms' tumour suppressor protein WT1.
A;Reference number: I58315; MUID:95166649; PMID:7862533
A;Accession: I58315
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'MGHHHHHHHHSSGHIEGRHM',301-364,'F',366-386,'T',388-407,411-449 <HAM>
A;Cross-references: UNIPARC:UPI0000072BDE; GB:S75264; NID:g896246; PIDN:AAB33443.1; PID:g896247
A;Note: this sequence is engineered
C;Genetics:
A;Gene: GDB:WT1
A;Cross-references: GDB:120496; OMIM:194070
A;Map position: 11p13-11p13
A;Introns: 148/1; 189/1; 223/2; 249/2; 266/2; 298/3; 349/1; 379/1; 410/1
A;Note: mRNA transcripts containing both alternatively spliced regions are the most abundant; those lacking both are the least abundant
C;Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger
F;1-449/Product: Wilms tumor susceptibility protein WT1, splice form 1 #status predicted <SF1>
F;1-407,411-449/Product: Wilms tumor susceptibility protein WT1, splice form 4 #status predicted <SF4>
F;1-249,267-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #status predicted <SF3>
F;1-249,267-407,411-449/Product: Wilms tumor susceptibility protein WT1, splice form 2 #status predicted <SF2>

Query Match 86.2%; Score 50; DB 2; Length 449;
Best Local Similarity 88.9%; Pred. No. 0.69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 235 CMTWNQMNL 243

RESULT 4
A39692
Wilms' tumor protein analog, WT1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 16-Feb-1997
C;Accession: A39692
R;Buckler, A.J.; Pelletier, J.; Haber, D.A.; Glaser, T.; Housman, D.E.
Mol. Cell. Biol. 11, 1707-1712, 1991
A;Title: Isolation, characterization, and expression of the murine Wilms' tumor gene (WT1) during kidney development.
A;Reference number: A39692; MUID:91141522; PMID:1671709
A;Accession: A39692
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-449 <BUC>
A;Cross-references: UNIPARC:UPI0000147984; GB:M55512
C;Keywords: alternative splicing; DNA binding; transcription regulation; tumor suppressor; zinc finger

Query Match 86.2%; Score 50; DB 2; Length 449;
Best Local Similarity 88.9%; Pred. No. 0.69;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 235 CMTWNQMNL 243

RESULT 5

G89999

conserved hypothetical protein SA1877 [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: G89999

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;

Oguchi, A.; Aoki, K.; Nagai, Y.; Lian, J.; Ito, T.; Kanamori, M.; Matsumaru, H.;

Maruyama, A.; Murakami, H.; Hosoyama, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.;

Inoue, R.; Kaito, C.; Sekimizu, K.; Hirakawa, H.; Kuhara, S.; Goto, S.; Yabuzaki, J.;

Kanehisa, M.; Yamashita, A.; Oshima, K.; Furuya, K.; Yoshino, C.; Shiba, T.; Hattori, M.;

Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: G89999

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-527 <KUR>

A;Cross-references: UNIPROT:Q9ZAH8; UNIPARC:UPI00000D77B0; GB:BA000018; PID:g13701868;

PIDN:BA43160.1; GSPDB:GN00149

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA1877

Query Match 67.2%; Score 39; DB 2; Length 527;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 408 CYFWNQLLL 416

RESULT 6

S68588

nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004

C;Accession: S68588; S57496

R;Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.

J. Mol. Biol. 258, 261-269, 1996

A;Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.

A;Reference number: S68587; MUID:96196478; PMID:8627624

A;Accession: S68588

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-498 <BAL>

A;Cross-references: UNIPROT:P48180; UNIPARC:UPI0000125225; EMBL:X83887; NID:g872087;

PIDN:CAA58764.1; PID:g872088

C;Superfamily: acetylcholine receptor

C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane; transmembrane protein

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT>

Query Match 65.5%; Score 38; DB 2; Length 498;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YTNQMNL 9

Db ||||| ||
77 YTWNDYNL 84

RESULT 7

AE0716

hypothetical protein STY1869 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0716
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Mungall, K.L.; Bentley, S.D.; Holden, M.T.G.; Sebaihia, M.; Baker, S.; Basham, D.; Brooks, K.; Chillingworth, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Feltwell, T.; Hamlin, N.; Haque, A.; Hien, T.T.; Holroyd, S.; Jagels, K.; Krogh, A.; Larsen, T.S.; Leather, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.G.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0716
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <PAR>
A;Cross-references: UNIPARC:UPI00000CDB46; GB:AL513382; PIDN:CAD02102.1; PID:g16502937; GSPDB:GN00176
C;Genetics:
A;Gene: STY1869

Query Match 63.8%; Score 37; DB 2; Length 347;
Best Local Similarity 62.5%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YTNQMNL 9
 ||||| :|
Db 332 YTNRKNI 339

RESULT 8

S63226

hypothetical protein YNL253w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0860
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 05-Oct-2004
C;Accession: S63226
R;Sen-Gupta, M.; Guedener, U.; Beinhauer, J.; Fiedler, T.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63220
A;Accession: S63226
A;Molecule type: DNA
A;Residues: 1-422 <SEN>
A;Cross-references: UNIPROT:P53851; UNIPARC:UPI000013BBD9; EMBL:Z71529; NID:g1302298; PID:e239643; PID:g1302299; GSPDB:GN00014; MIPS:YNL253w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNL253w
A;Cross-references: SGD:S0005197
A;Map position: 14L

Query Match 63.8%; Score 37; DB 2; Length 422;
Best Local Similarity 55.6%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CYTNQMNL 9
 || || :|
Db 277 CYVWNMKS 285

RESULT 9

G83933

dipeptidase BH2271 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: G83933

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiram, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: G83933

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-310 <STO>

A;Cross-references: UNIPROT:Q9KAL6; UNIPARC:UPI00000C3E6A; GB:AP001515; GB:BA000004;

NID:g10174886; PIDN:BAB05990.1; GSPDB:GN00137

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2271

C;Superfamily: membrane dipeptidase

Query Match 62.1%; Score 36; DB 2; Length 310;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TWNQMNL 9
||| ||
Db 130 TWNQANL 136

RESULT 10

S59801

protein kinase SSK2 (EC 2.7.1.-) - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein N3276; protein YNR031c

C;Species: *Saccharomyces cerevisiae*

C;Date: 13-Jan-1996 #sequence_revision 23-Feb-1996 #text_change 05-Oct-2004

C;Accession: S59801; S63362

R;Maeda, T.; Takekawa, M.; Saito, H.

Science 269, 554-558, 1995

A;Title: Activation of yeast PBS2 MAPKK by MAPKKs or by binding of an SH3-containing osmosensor.

A;Reference number: S59801; MUID:95350642; PMID:7624781

A;Accession: S59801

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-1579 <MAE>

A;Cross-references: UNIPROT:P53599; UNIPARC:UPI0000135FDB; EMBL:L41927; NID:g940329;

PIDN:AAC41665.1; PID:g940330

R;Pohl, T.M.

submitted to the Protein Sequence Database, April 1996

A;Reference number: S63346

A;Accession: S63362

A;Molecule type: DNA

A;Residues: 1-1579 <POH>

A;Cross-references: UNIPARC:UPI0000135FDB; EMBL:Z71646; NID:g1302526; PIDN:CAA96311.1;

PID:e239826; PID:g1302527; MIPS:YNR031c

A;Experimental source: strain S288C

C;Genetics:

A;Gene: SGD:SSK2

A;Cross-references: SGD:S0005314; MIPS:YNR031c

A;Map position: 14R

C;Keywords: ATP; phosphotransferase; protein kinase

F;1264-1558/Domain: protein kinase homology <KIN>

F;1272-1280/Region: protein kinase ATP-binding motif

Query Match 62.1%; Score 36; DB 2; Length 1579;
Best Local Similarity 71.4%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Sugiyama 10 527 692 PG-PUBs, "New" file

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2007, 07:44:31 ; Search time 144 Seconds
(without alignments)
11.986 Million cell updates/sec

Title: US-10-527-692-3
Perfect score: 58
Sequence: 1 CYTWNQMN 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 848676 seqs, 191783220 residues

Total number of hits satisfying chosen parameters: 848676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	58	100.0	9	6	US-10-482-327-9	Sequence 9, Appli
2	58	100.0	9	6	US-10-528-360-3	Sequence 3, Appli
3	58	100.0	9	6	US-10-541-821-44	Sequence 44, Appl
4	50	86.2	9	6	US-10-482-327-7	Sequence 7, Appli
5	50	86.2	9	6	US-10-528-360-2	Sequence 2, Appli
6	50	86.2	9	6	US-10-541-821-11	Sequence 11, Appl
7	50	86.2	9	7	US-11-322-245-7	Sequence 7, Appli
8	50	86.2	9	7	US-11-340-431-49	Sequence 49, Appl
9	50	86.2	9	7	US-11-340-431-258	Sequence 258, App
10	50	86.2	9	7	US-11-540-317-49	Sequence 49, Appl
11	50	86.2	9	7	US-11-540-317-258	Sequence 258, App
12	50	86.2	302	7	US-11-371-354-65533	Sequence 65533, A
13	50	86.2	432	7	US-11-090-997-1828	Sequence 1828, Ap
14	50	86.2	432	7	US-11-090-997-1910	Sequence 1910, Ap
15	50	86.2	449	6	US-10-482-327-1	Sequence 1, Appli
16	50	86.2	449	6	US-10-482-327-2	Sequence 2, Appli
17	50	86.2	449	6	US-10-528-360-1	Sequence 1, Appli
18	50	86.2	449	6	US-10-541-821-1	Sequence 1, Appli
19	50	86.2	449	7	US-11-322-245-1	Sequence 1, Appli
20	50	86.2	449	7	US-11-322-245-2	Sequence 2, Appli
21	50	86.2	449	7	US-11-340-431-319	Sequence 319, App

22	50	86.2	449	7	US-11-340-431-320	Sequence 320, App
23	50	86.2	449	7	US-11-090-997-1826	Sequence 1826, Ap
24	50	86.2	449	7	US-11-090-997-1912	Sequence 1912, Ap
25	50	86.2	449	7	US-11-540-317-319	Sequence 319, App
26	50	86.2	449	7	US-11-540-317-320	Sequence 320, App
27	49	84.5	9	6	US-10-528-360-5	Sequence 5, Appli
28	49	84.5	9	6	US-10-528-360-6	Sequence 6, Appli
29	49	84.5	9	6	US-10-528-360-7	Sequence 7, Appli
30	49	84.5	9	6	US-10-528-360-8	Sequence 8, Appli
31	49	84.5	9	6	US-10-528-360-9	Sequence 9, Appli
32	49	84.5	9	6	US-10-528-360-10	Sequence 10, Appl
33	49	84.5	9	6	US-10-528-360-11	Sequence 11, Appl
34	49	84.5	9	6	US-10-528-360-12	Sequence 12, Appl
35	49	84.5	9	6	US-10-528-360-13	Sequence 13, Appl
36	49	84.5	9	6	US-10-528-360-14	Sequence 14, Appl
37	46	79.3	9	6	US-10-541-821-72	Sequence 72, Appl
38	42	72.4	9	6	US-10-528-360-4	Sequence 4, Appli
39	42	72.4	9	6	US-10-528-360-15	Sequence 15, Appl
40	42	72.4	9	6	US-10-528-360-16	Sequence 16, Appl
41	42	72.4	9	6	US-10-528-360-17	Sequence 17, Appl
42	42	72.4	9	6	US-10-528-360-18	Sequence 18, Appl
43	42	72.4	9	6	US-10-528-360-19	Sequence 19, Appl
44	42	72.4	9	6	US-10-528-360-20	Sequence 20, Appl
45	42	72.4	9	6	US-10-528-360-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-10-482-327-9

; Sequence 9, Application US/10482327

; Publication No. US20060165708A1

; GENERAL INFORMATION:

; APPLICANT: Tadanori Mayumi et al.

; TITLE OF INVENTION: Cancer Vaccine Comprising a Cancer Antigen Based on

; TITLE OF INVENTION: the Product of a Tumor Suppressor Gene WT1 and a Cationic

; TITLE OF INVENTION: Liposome

; FILE REFERENCE: K807

; CURRENT APPLICATION NUMBER: US/10/482,327

; CURRENT FILING DATE: 2003-12-29

; NUMBER OF SEQ ID NOS: 9

; SEQ ID NO 9

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Peptide

US-10-482-327-9

Query Match 100.0%; Score 58; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

|||||||

Db 1 CYTWNQMNL 9

RESULT 2

US-10-528-360-3

; Sequence 3, Application US/10528360

; Publication No. US20060205667A1

; GENERAL INFORMATION:

; APPLICANT: SUGIYAMA, Haruo

; APPLICANT: GOTOH, Masashi

; APPLICANT: TAKASU, Hideo

; APPLICANT: SAMIZO, Fumio

; APPLICANT: KUSUNOSE, Naoto

; APPLICANT: NAKATSUKA, Masashi

; TITLE OF INVENTION: SUBSTITUTED TYPE PEPTIDES OF WT1

```

; FILE REFERENCE: 0020-5357PUS1
; CURRENT APPLICATION NUMBER: US/10/528,360
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: PCT/JP2003/011974
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-528-360-3

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```

Query Match          100.0%; Score 58; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches      9; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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```

Qy      1 CYTWNQMNL 9
        |||||
Db      1 CYTWNQMNL 9

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RESULT 3

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US-10-541-821-44
; Sequence 44, Application US/10541821
; Publication No. US20060217297A1
; GENERAL INFORMATION:
; APPLICANT: Sugiyama, Haruo
; APPLICANT: Takasu, Hideo
; APPLICANT: Samizo, Fumio
; TITLE OF INVENTION: DIMERIZED PEPTIDE
; FILE REFERENCE: 283125US0XPCT
; CURRENT APPLICATION NUMBER: US/10/541,821
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: JP 2003-007122
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-541-821-44

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Query Match          100.0%; Score 58; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches      9; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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Qy      1 CYTWNQMNL 9
        |||||
Db      1 CYTWNQMNL 9

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RESULT 4

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US-10-482-327-7
; Sequence 7, Application US/10482327
; Publication No. US20060165708A1
; GENERAL INFORMATION:
; APPLICANT: Tadanori Mayumi et al.
; TITLE OF INVENTION: Cancer Vaccine Comprising a Cancer Antigen Based on
; TITLE OF INVENTION: the Product of a Tumor Suppressor Gene Wt1 and a Cationic
; TITLE OF INVENTION: Liposome
; FILE REFERENCE: K807
; CURRENT APPLICATION NUMBER: US/10/482,327
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 9

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; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-482-327-7

Query Match 86.2%; Score 50; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 1 CMTWNQMNL 9

RESULT 5

US-10-528-360-2

; Sequence 2, Application US/10528360
; Publication No. US20060205667A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, Haruo
; APPLICANT: GOTOH, Masashi
; APPLICANT: TAKASU, Hideo
; APPLICANT: SAMIZO, Fumio
; APPLICANT: KUSUNOSE, Naoto
; APPLICANT: NAKATSUKA, Masashi
; TITLE OF INVENTION: SUBSTITUTED TYPE PEPTIDES OF WT1
; FILE REFERENCE: 0020-5357PUS1
; CURRENT APPLICATION NUMBER: US/10/528,360
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: PCT/JP2003/011974
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-528-360-2

Query Match 86.2%; Score 50; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 1 CMTWNQMNL 9

RESULT 6

US-10-541-821-11

; Sequence 11, Application US/10541821
; Publication No. US20060217297A1
; GENERAL INFORMATION:
; APPLICANT: Sugiyama, Haruo
; APPLICANT: Takasu, Hideo
; APPLICANT: Samizo, Fumio
; TITLE OF INVENTION: DIMERIZED PEPTIDE
; FILE REFERENCE: 283125US0XPCT
; CURRENT APPLICATION NUMBER: US/10/541,821
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: JP 2003-007122
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-541-821-11

Query Match 86.2%; Score 50; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 1 CMTWNQMNL 9

RESULT 7

US-11-322-245-7
; Sequence 7, Application US/11322245
; Publication No. US20060093615A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, HARUO
; APPLICANT: OKA, YOSHIHIRO
; TITLE OF INVENTION: TUMOR ANTIGEN BASED ON PRODUCTS OF THE TUMOR SUPPRESSOR
; TITLE OF INVENTION: GENE WT1
; FILE REFERENCE: 053466/0298
; CURRENT APPLICATION NUMBER: US/11/322,245
; CURRENT FILING DATE: 2006-01-03
; PRIOR APPLICATION NUMBER: US/09/744,815
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/JP99/04130
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: JP 10-218093
; PRIOR FILING DATE: 1998-07-31
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-322-245-7

Query Match 86.2%; Score 50; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 1 CMTWNQMNL 9

RESULT 8

US-11-340-431-49
; Sequence 49, Application US/11340431
; Publication No. US20060121046A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C13
; CURRENT APPLICATION NUMBER: US/11/340,431
; CURRENT FILING DATE: 2006-01-25
; PRIOR APPLICATION NUMBER: US 09/164,223
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Homo sapiens
US-11-340-431-49

Query Match 86.2%; Score 50; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 1 CMTWNQMNL 9

RESULT 9

US-11-340-431-258
; Sequence 258, Application US/11340431
; Publication No. US20060121046A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1 SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C13
; CURRENT APPLICATION NUMBER: US/11/340,431
; CURRENT FILING DATE: 2006-01-25
; PRIOR APPLICATION NUMBER: US 09/164,223
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 258
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-340-431-258

Query Match 86.2%; Score 50; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 1 CMTWNQMNL 9

RESULT 10

US-11-540-317-49
; Sequence 49, Application US/11540317
; Publication No. US20070026008A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C14
; CURRENT APPLICATION NUMBER: US/11/540,317
; CURRENT FILING DATE: 2006-09-28
; PRIOR APPLICATION NUMBER: US 09/684,361
; PRIOR FILING DATE: 2006-10-06
; PRIOR APPLICATION NUMBER: US 09/276,484
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/164,223
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-540-317-49

Query Match 86.2%; Score 50; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 1 CMTWNQMNL 9

RESULT 11

US-11-540-317-258
; Sequence 258, Application US/11540317
; Publication No. US20070026008A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C14
; CURRENT APPLICATION NUMBER: US/11/540,317
; CURRENT FILING DATE: 2006-09-28
; PRIOR APPLICATION NUMBER: US 09/684,361
; PRIOR FILING DATE: 2006-10-06
; PRIOR APPLICATION NUMBER: US 09/276,484
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/164,223
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 258
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-540-317-258

Query Match 86.2%; Score 50; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 1 CMTWNQMNL 9

RESULT 12

US-11-371-354-65533
; Sequence 65533, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65533
; LENGTH: 302

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-65533

Query Match 86.2%; Score 50; DB 7; Length 302;
Best Local Similarity 88.9%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
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Db 91 CMTWNQMNL 99

RESULT 13

US-11-090-997-1828
; Sequence 1828, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betsholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1828
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-090-997-1828

Query Match 86.2%; Score 50; DB 7; Length 432;
Best Local Similarity 88.9%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
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Db 235 CMTWNQMNL 243

RESULT 14

US-11-090-997-1910
; Sequence 1910, Application US/11090997
; Publication No. US20060216722A1
; GENERAL INFORMATION:
; APPLICANT: Betsholtz, Christer et. al.
; TITLE OF INVENTION: Glomerular Expression Profiling
; FILE REFERENCE: 04-1059
; CURRENT APPLICATION NUMBER: US/11/090,997
; CURRENT FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2985
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1910
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-997-1910

Query Match 86.2%; Score 50; DB 7; Length 432;
Best Local Similarity 88.9%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 235 CMTWNQMNL 243

RESULT 15

US-10-482-327-1
; Sequence 1, Application US/10482327
; Publication No. US20060165708A1

; GENERAL INFORMATION:
; APPLICANT: Tadanori Mayumi et al.
; TITLE OF INVENTION: Cancer Vaccine Comprising a Cancer Antigen Based on
; TITLE OF INVENTION: the Product of a Tumor Suppressor Gene Wt1 and a Cationic
; TITLE OF INVENTION: Liposome
; FILE REFERENCE: K807
; CURRENT APPLICATION NUMBER: US/10/482,327
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 1
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Mouse
US-10-482-327-1

Query Match 86.2%; Score 50; DB 6; Length 449;
Best Local Similarity 88.9%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 235 CMTWNQMNL 243

Search completed: March 17, 2007, 07:46:55
Job time : 144 secs

Sugiyama 10527692 RAI search = Issued Patents

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2007, 07:36:07 ; Search time 116 Seconds
(without alignments)
6.791 Million cell updates/sec

Title: US-10-527-692-3
Perfect score: 58
Sequence: 1 CYTWNQMNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	50	86.2	9	3	US-09-744-815-7	Sequence 7, Appli
2	50	86.2	345	1	US-08-102-942A-2	Sequence 2, Appli
3	50	86.2	345	2	US-09-037-179B-2	Sequence 2, Appli
4	50	86.2	345	2	US-09-929-315-2	Sequence 2, Appli
5	50	86.2	429	1	US-08-234-783-4	Sequence 4, Appli
6	50	86.2	429	1	US-08-456-907-4	Sequence 4, Appli
7	50	86.2	429	5	PCT-US95-05523-4	Sequence 4, Appli
8	50	86.2	449	1	US-08-102-942A-4	Sequence 4, Appli
9	50	86.2	449	1	US-08-102-942A-6	Sequence 6, Appli
10	50	86.2	449	2	US-09-037-179B-4	Sequence 4, Appli
11	50	86.2	449	2	US-09-037-179B-6	Sequence 6, Appli
12	50	86.2	449	2	US-09-538-092-960	Sequence 960, App
13	50	86.2	449	2	US-09-929-315-4	Sequence 4, Appli
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16	50	86.2	449	3	US-09-744-815-2	Sequence 2, Appli
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18	50	86.2	559	2	US-09-949-016-9139	Sequence 9139, Ap
19	50	86.2	559	2	US-09-949-016-9140	Sequence 9140, Ap
20	50	86.2	559	2	US-09-949-016-9141	Sequence 9141, Ap
21	50	86.2	576	2	US-09-949-016-9404	Sequence 9404, Ap
22	50	86.2	576	2	US-09-949-016-9405	Sequence 9405, Ap

23	50	86.2	576	2	US-09-949-016-9406	Sequence 9406, Ap
24	50	86.2	576	2	US-09-949-016-9407	Sequence 9407, Ap
25	50	86.2	578	3	US-09-684-215B-8	Sequence 8, Appli
26	36	62.1	163	2	US-10-094-749-3214	Sequence 3214, Ap
27	36	62.1	1579	2	US-09-487-558B-368	Sequence 368, App
28	35	60.3	50	2	US-09-270-767-37884	Sequence 37884, A
29	35	60.3	50	2	US-09-270-767-53101	Sequence 53101, A
30	35	60.3	68	2	US-09-583-110-4302	Sequence 4302, Ap
31	35	60.3	68	2	US-09-107-433-5009	Sequence 5009, Ap
32	35	60.3	72	2	US-09-583-110-4301	Sequence 4301, Ap
33	35	60.3	72	2	US-09-107-433-4135	Sequence 4135, Ap
34	35	60.3	143	2	US-09-538-092-237	Sequence 237, App
35	35	60.3	154	1	US-08-102-942A-5	Sequence 5, Appli
36	35	60.3	154	2	US-09-037-179B-5	Sequence 5, Appli
37	35	60.3	154	2	US-09-929-315-5	Sequence 5, Appli
38	35	60.3	223	2	US-09-248-796A-20910	Sequence 20910, A
39	35	60.3	575	2	US-09-171-461-7	Sequence 7, Appli
40	35	60.3	575	2	US-09-970-711-7	Sequence 7, Appli
41	35	60.3	769	2	US-09-248-796A-16368	Sequence 16368, A
42	35	60.3	938	2	US-08-897-843A-1	Sequence 1, Appli
43	35	60.3	1770	2	US-09-827-998-10	Sequence 10, Appl
44	35	60.3	1791	2	US-09-827-998-3	Sequence 3, Appli
45	34	58.6	73	2	US-09-248-796A-23443	Sequence 23443, A

ALIGNMENTS

RESULT 1

US-09-744-815-7

; Sequence 7, Application US/09744815

; Patent No. 7030212

; GENERAL INFORMATION:

; APPLICANT: SUGIYAMA, HARUO

; APPLICANT: OKA, YOSHIHIRO

; TITLE OF INVENTION: TUMOR ANTIGEN BASED ON PRODUCTS OF THE TUMOR SUPPRESSOR

; TITLE OF INVENTION: GENE WT1

; FILE REFERENCE: 053466/0298

; CURRENT APPLICATION NUMBER: US/09/744,815

; CURRENT FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: PCT/JP99/04130

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: JP 10-218093

; PRIOR FILING DATE: 1998-07-31

; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 7

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-09-744-815-7

Query Match 86.2%; Score 50; DB 3; Length 9;

Best Local Similarity 88.9%; Pred. No. 5e+05;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

| | | | | | | |

Db 1 CMTWNQMNL 9

RESULT 2

US-08-102-942A-2

; Sequence 2, Application US/08102942A

; Patent No. 5726288

; GENERAL INFORMATION:

; APPLICANT: Call, Katherine M.

; APPLICANT: Glaser, Thomas M.

; APPLICANT: Ito, Caryn Y.


```

; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-102-942A-2.

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Query Match      86.2%; Score 50; DB 1; Length 345;
Best Local Similarity 88.9%; Pred. No. 0.95;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

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Qy      1 CYTWNQMNL 9
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Db      151 CMTWNQMNL 159

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RESULT 3
US-09-037-179B-2
; Sequence 2, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942

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; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-037-179B-2
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Query Match      86.2%; Score 50; DB 2; Length 345;
Best Local Similarity 88.9%; Pred. No. 0.95;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
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Qy      1 CYTWNQMNL 9
        | |||||
Db      151 CMTWNQMNL 159
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```
RESULT 4
US-09-929-315-2
; Sequence 2, Application US/09929315
; Patent No. 6943011
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-013
; CURRENT APPLICATION NUMBER: US/09/929,315
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/037,179
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1991-11-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-929-315-2
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Query Match      86.2%; Score 50; DB 2; Length 345;
Best Local Similarity 88.9%; Pred. No. 0.95;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
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Qy      1 CYTWNQMNL 9
        | |||||
Db      151 CMTWNQMNL 159
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RESULT 5
 US-08-234-783-4
 ; Sequence 4, Application US/08234783
 ; Patent No. 5622835
 ; GENERAL INFORMATION:
 ; APPLICANT: Herlyn, Meenhard
 ; APPLICANT: Morris, Jennifer
 ; APPLICANT: Rauscher III, Frank J.
 ; APPLICANT: Rodeck, Ulrich
 ; TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of
 ; TITLE OF INVENTION: Use Therefor
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, PO Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/234,783
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bak, Mary E.
 ; REGISTRATION NUMBER: 31,215
 ; REFERENCE/DOCKET NUMBER: WST48USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-540-9200
 ; TELEFAX: 215-540-5818
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 429 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-234-783-4

Query Match 86.2%; Score 50; DB 1; Length 429;
 Best Local Similarity 88.9%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 235 CMTWNQMNL 243

RESULT 6
 US-08-456-907-4
 ; Sequence 4, Application US/08456907
 ; Patent No. 5633142
 ; GENERAL INFORMATION:
 ; APPLICANT: Herlyn, Meenhard
 ; APPLICANT: Morris, Jennifer
 ; APPLICANT: Rauscher III, Frank J.
 ; APPLICANT: Rodeck, Ulrich
 ; TITLE OF INVENTION: WT1 Monoclonal Antibodies and Methods of
 ; TITLE OF INVENTION: Use Therefor
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howson and Howson
 ; STREET: Spring House Corporate Cntr, PO Box 457
 ; CITY: Spring House
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19477

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,907
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-456-907-4

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Query Match          86.2%; Score 50; DB 1; Length 429;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches      8; Conservative    0; Mismatches    1; Indels    0; Gaps    0;

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```

Qy      1 CYTWNQMNL 9
        | |||||
Db      235 CMTWNQMNL 243

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RESULT 7
PCT-US95-05523-4
; Sequence 4, Application PC/TUS9505523
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of Anatomy and Biology
; TITLE OF INVENTION: WT1 Monoclonal Antibodies and
; TITLE OF INVENTION: Methods of Use Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,783
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST48PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-05523-4

Query Match 86.2%; Score 50; DB 5; Length 429;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 235 CMTWNQMNL 243

RESULT 8

US-08-102-942A-4

; Sequence 4, Application US/08102942A

; Patent No. 5726288

; GENERAL INFORMATION:

; APPLICANT: Call, Katherine M.

; APPLICANT: Glaser, Thomas M.

; APPLICANT: Ito, Caryn Y.

; APPLICANT: Buckler, Alan J.

; APPLICANT: Pelletier, Jerry

; APPLICANT: Haber, Daniel A.

; APPLICANT: Rose, Elise A.

; APPLICANT: Housman, David E.

; APPLICANT: Bruening, Wendy

; APPLICANT: Darveau, Andre

; TITLE OF INVENTION: Localization and Characterization of the

; TITLE OF INVENTION: Wilms' Tumor Gene

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: U.S.

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/102,942A

; FILING DATE: 02-AUG-1993

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: MIT-5194A2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 449 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-102-942A-4

Query Match 86.2%; Score 50; DB 1; Length 449;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||

Db 235 CMTWNQMNL 243

RESULT 9

US-08-102-942A-6

; Sequence 6, Application US/08102942A

; Patent No. 5726288

; GENERAL INFORMATION:

; APPLICANT: Call, Katherine M.

; APPLICANT: Glaser, Thomas M.

; APPLICANT: Ito, Caryn Y.

; APPLICANT: Buckler, Alan J.

; APPLICANT: Pelletier, Jerry

; APPLICANT: Haber, Daniel A.

; APPLICANT: Rose, Elise A.

; APPLICANT: Housman, David E.

; APPLICANT: Bruening, Wendy

; APPLICANT: Darveau, Andre

; TITLE OF INVENTION: Localization and Characterization of the

; TITLE OF INVENTION: Wilms' Tumor Gene

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: Massachusetts

; COUNTRY: U.S.

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/102,942A

; FILING DATE: 02-AUG-1993

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: MIT-5194A2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 449 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-102-942A-6

Query Match 86.2%; Score 50; DB 1; Length 449;

Best Local Similarity 88.9%; Pred. No. 1.2;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

| | | | | | | |

Db 235 CMTWNQMNL 243

RESULT 10

US-09-037-179B-4

; Sequence 4, Application US/09037179B

; Patent No. 6316599

; GENERAL INFORMATION:

; APPLICANT: Call, Katherine M.

; APPLICANT: Glaser, Thomas M.

; APPLICANT: Ito, Caryn Y.

; APPLICANT: Buckler, Alan J.

```
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine
US-09-037-179B-4
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Query.Match      86.2%; Score 50; DB 2; Length 449;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
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Qy      1 CYTWNQMNL 9
        | |||||
Db      235 CMTWNQMNL 243
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RESULT 11

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US-09-037-179B-6
; Sequence 6, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; CURRENT FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 449
; TYPE: PRT
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; ORGANISM: Homo sapien
US-09-037-179B-6

Query Match 86.2%; Score 50; DB 2; Length 449;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 235 CMTWNQMNL 243

RESULT 12

US-09-538-092-960
; Sequence 960, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 960
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P19544
US-09-538-092-960

Query Match 86.2%; Score 50; DB 2; Length 449;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 235 CMTWNQMNL 243

RESULT 13

US-09-929-315-4
; Sequence 4, Application US/09929315
; Patent No. 6943011
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-013
; CURRENT APPLICATION NUMBER: US/09/929,315
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/037,179
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942


```
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1991-11-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine
US-09-929-315-4
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Query Match      86.2%; Score 50; DB 2; Length 449;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      1 CYTWNQMNL 9
        | |||||
Db      235 CMTWNQMNL 243
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RESULT 14

US-09-929-315-6

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; Sequence 6, Application US/09929315
; Patent No. 6943011
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; FILE REFERENCE: 0050.1312-013
; CURRENT APPLICATION NUMBER: US/09/929,315
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/037,179
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1991-11-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-929-315-6
```

```
Query Match      86.2%; Score 50; DB 2; Length 449;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
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Qy      1 CYTWNQMNL 9
        | |||||
Db      235 CMTWNQMNL 243
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RESULT 15
 US-09-744-815-1
 ; Sequence 1, Application US/09744815
 ; Patent No. 7030212
 ; GENERAL INFORMATION:
 ; APPLICANT: SUGIYAMA, HARUO
 ; APPLICANT: OKA, YOSHIHIRO
 ; TITLE OF INVENTION: TUMOR ANTIGEN BASED ON PRODUCTS OF THE TUMOR SUPPRESSOR
 ; TITLE OF INVENTION: GENE WT1
 ; FILE REFERENCE: 053466/0298
 ; CURRENT APPLICATION NUMBER: US/09/744,815
 ; CURRENT FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: PCT/JP99/04130
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: JP 10-218093
 ; PRIOR FILING DATE: 1998-07-31
 ; NUMBER OF SEQ ID NOS: 8
 ; SEQ ID NO 1
 ; LENGTH: 449
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-744-815-1

Query Match 86.2%; Score 50; DB 3; Length 449;
 Best Local Similarity 88.9%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 235 CMTWNQMNL 243

Search completed: March 17, 2007, 07:38:04
 Job time : 116 secs

Sugiyama 10527692 PG-PUBS search = AA Main database

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2007, 07:38:10 ; Search time 405 Seconds
(without alignments)
10.294 Million cell updates/sec

Title: US-10-527-692-3
Perfect score: 58
Sequence: 1 CYTWNQMNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	58	100.0	9	4	US-10-471-835-3	Sequence 3, Appli
2	58	100.0	9	5	US-10-490-873-4	Sequence 4, Appli
3	58	100.0	9	5	US-10-490-865-4	Sequence 4, Appli
4	50	86.2	9	3	US-09-938-864-49	Sequence 49, Appl
5	50	86.2	9	3	US-09-938-864-258	Sequence 258, App
6	50	86.2	9	3	US-09-791-477-49	Sequence 49, Appl
7	50	86.2	9	3	US-09-791-477-258	Sequence 258, App
8	50	86.2	9	3	US-09-785-019-49	Sequence 49, Appl
9	50	86.2	9	3	US-09-785-019-258	Sequence 258, App
10	50	86.2	9	4	US-10-125-635A-49	Sequence 49, Appl
11	50	86.2	9	4	US-10-125-635A-258	Sequence 258, App
12	50	86.2	9	4	US-10-002-603-49	Sequence 49, Appl
13	50	86.2	9	4	US-10-002-603-258	Sequence 258, App
14	50	86.2	9	4	US-10-195-835-49	Sequence 49, Appl
15	50	86.2	9	4	US-10-195-835-258	Sequence 258, App
16	50	86.2	9	4	US-10-286-333-49	Sequence 49, Appl
17	50	86.2	9	4	US-10-286-333-258	Sequence 258, App
18	50	86.2	9	4	US-10-244-830-49	Sequence 49, Appl
19	50	86.2	9	4	US-10-244-830-258	Sequence 258, App
20	50	86.2	9	4	US-10-427-717-49	Sequence 49, Appl
21	50	86.2	9	4	US-10-427-717-258	Sequence 258, App
22	50	86.2	9	4	US-10-471-835-2	Sequence 2, Appli
23	50	86.2	9	4	US-10-648-780-49	Sequence 49, Appl

24	50	86.2	9	4	US-10-648-780-258	Sequence 258, App
25	50	86.2	9	5	US-10-490-873-3	Sequence 3, Appli
26	50	86.2	9	5	US-10-490-865-3	Sequence 3, Appli
27	50	86.2	9	5	US-10-999-425-33	Sequence 33, Appl
28	50	86.2	9	6	US-11-196-459-7	Sequence 7, Appli
29	50	86.2	9	6	US-11-223-139-33	Sequence 33, Appl
30	50	86.2	133	3	US-09-938-864-344	Sequence 344, App
31	50	86.2	133	3	US-09-785-019-344	Sequence 344, App
32	50	86.2	133	4	US-10-125-635A-344	Sequence 344, App
33	50	86.2	133	4	US-10-002-603-344	Sequence 344, App
34	50	86.2	133	4	US-10-195-835-344	Sequence 344, App
35	50	86.2	133	4	US-10-286-333-344	Sequence 344, App
36	50	86.2	133	4	US-10-244-830-344	Sequence 344, App
37	50	86.2	133	4	US-10-427-717-344	Sequence 344, App
38	50	86.2	133	4	US-10-648-780-344	Sequence 344, App
39	50	86.2	214	3	US-09-938-864-395	Sequence 395, App
40	50	86.2	214	4	US-10-125-635A-395	Sequence 395, App
41	50	86.2	214	4	US-10-002-603-395	Sequence 395, App
42	50	86.2	214	4	US-10-195-835-395	Sequence 395, App
43	50	86.2	214	4	US-10-286-333-395	Sequence 395, App
44	50	86.2	214	4	US-10-244-830-395	Sequence 395, App
45	50	86.2	214	4	US-10-427-717-395	Sequence 395, App

ALIGNMENTS

RESULT 1

US-10-471-835-3

; Sequence 3, Application US/10471835

; Publication No. US20040097703A1

; GENERAL INFORMATION:

; APPLICANT: Haruo Sugiyama

; TITLE OF INVENTION: Wt1 modified peptide

; FILE REFERENCE: J939

; CURRENT APPLICATION NUMBER: US/10/471,835

; CURRENT FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: JP 2001-83250

; PRIOR FILING DATE: 2001-03-22

; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 3

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Peptide

US-10-471-835-3

Query Match 100.0%; Score 58; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

|||||||

Db 1 CYTWNQMNL 9

RESULT 2

US-10-490-873-4

; Sequence 4, Application US/10490873

; Publication No. US20040247609A1

; GENERAL INFORMATION:

; APPLICANT: SUGIYAMA, Haruo

; TITLE OF INVENTION: NOVEL METHODS OF INDUCING ANTIGEN-SPECIFIC T CELLS

; FILE REFERENCE: 0020-5247PUS1

; CURRENT APPLICATION NUMBER: US/10/490,873

; CURRENT FILING DATE: 2004-06-17

; PRIOR APPLICATION NUMBER: PCT/JP02/09993

; PRIOR FILING DATE: 2002-09-27

; NUMBER OF SEQ ID NOS: 8

; SEQ ID NO 4

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-490-873-4

Query Match 100.0%; Score 58; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 1 CYTWNQMNL 9

RESULT 3

US-10-490-865-4

; Sequence 4, Application US/10490865
; Publication No. US20050002951A1
; GENERAL INFORMATION:
; APPLICANT: SUGIYAMA, Haruo
; APPLICANT: AZUMA, Ichiro
; TITLE OF INVENTION: Methods for Inducing Antigen-Specific T Cells
; FILE REFERENCE: 0020-5246PUS1
; CURRENT APPLICATION NUMBER: US/10/490,865
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: PCT/JP02/09997
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-490-865-4

Query Match 100.0%; Score 58; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 1 CYTWNQMNL 9

RESULT 4

US-09-938-864-49

; Sequence 49, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-49

Query Match 86.2%; Score 50; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | |
Db 1 CMTWNQMNL 9

RESULT 5

US-09-938-864-258
; Sequence 258, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 258
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-938-864-258

Query Match 86.2%; Score 50; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | |
Db 1 CMTWNQMNL 9

RESULT 6

US-09-791-477-49
; Sequence 49, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-791-477-49

Query Match 86.2%; Score 50; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 1 CMTWNQMNL 9

RESULT 7

US-09-791-477-258

; Sequence 258, Application US/09791477
; Publication No. US20030082194A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA
; FILE REFERENCE: 2077.000200
; CURRENT APPLICATION NUMBER: US/09/791,477
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,070
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 258
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-477-258

Query Match 86.2%; Score 50; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| |||||
Db 1 CMTWNQMNL 9

RESULT 8

US-09-785-019-49

; Sequence 49, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-785-019-49

Query Match 86.2%; Score 50; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 1 CMTWNQMNL 9

RESULT 9

US-09-785-019-258
; Sequence 258, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 258
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-785-019-258

Query Match 86.2%; Score 50; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 1 CMTWNQMNL 9

RESULT 10

US-10-125-635A-49
; Sequence 49, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-125-635A-49

Query Match 86.2%; Score 50; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 1 CMTWNQMNL 9

RESULT 11

US-10-125-635A-258
 ; Sequence 258, Application US/10125635A
 ; Publication No. US20030039635A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C7
 ; CURRENT APPLICATION NUMBER: US/10/125,635A
 ; CURRENT FILING DATE: 2002-07-19
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 258
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-125-635A-258

Query Match 86.2%; Score 50; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.9e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 1 CMTWNQMNL 9

RESULT 12

US-10-002-603-49
 ; Sequence 49, Application US/10002603
 ; Publication No. US20030095971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Smithgall, Molly
 ; APPLICANT: Moulton, Gus
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Mossman, Sally
 ; APPLICANT: Evans, Lawrence
 ; APPLICANT: Spies, A. Gregory
 ; APPLICANT: Boydston, Jeremy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C6
 ; CURRENT APPLICATION NUMBER: US/10/002,603
 ; CURRENT FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 49
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-002-603-49

Query Match 86.2%; Score 50; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.9e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 1 CMTWNQMNL 9

RESULT 13

US-10-002-603-258

; Sequence 258, Application US/10002603

; Publication No. US20030095971A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Smithgall, Molly

; APPLICANT: Moulton, Gus

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Sleath, Paul R.

; APPLICANT: Mossman, Sally

; APPLICANT: Evans, Lawrence

; APPLICANT: Spies, A. Gregory

; APPLICANT: Boydston, Jeremy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

; FILE REFERENCE: 210121.465C6

; CURRENT APPLICATION NUMBER: US/10/002,603

; CURRENT FILING DATE: 2001-10-30

; NUMBER OF SEQ ID NOS: 413

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 258

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-002-603-258

Query Match 86.2%; Score 50; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.9e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

| | | | |

Db 1 CMTWNQMNL 9

RESULT 14

US-10-195-835-49

; Sequence 49, Application US/10195835

; Publication No. US20030198622A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Smithgall, Molly D.

; APPLICANT: Carter, Darrick

; APPLICANT: Cheever, Martin A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Sutherland, R. Alec

; APPLICANT: Mossman, Sally P.

; APPLICANT: Evans, Lawrence S.

; APPLICANT: Swanson, Ryan M.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

; FILE REFERENCE: 210121.465C8

; CURRENT APPLICATION NUMBER: US/10/195,835

; CURRENT FILING DATE: 2002-07-12

; NUMBER OF SEQ ID NOS: 461

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 49

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-195-835-49

Query Match 86.2%; Score 50; DB 4; Length 9;

Best Local Similarity 88.9%; Pred. No. 1.9e+06;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9

| | | | |

Db 1 CMTWNQMNL 9

RESULT 15
 US-10-195-835-258
 ; Sequence 258, Application US/10195835
 ; Publication No. US20030198622A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Smithgall, Molly D.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Sutherland, R. Alec
 ; APPLICANT: Mossman, Sally P.
 ; APPLICANT: Evans, Lawrence S.
 ; APPLICANT: Swanson, Ryan M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
 ; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
 ; FILE REFERENCE: 210121.465C8
 ; CURRENT APPLICATION NUMBER: US/10/195,835
 ; CURRENT FILING DATE: 2002-07-12
 ; NUMBER OF SEQ ID NOS: 461
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 258
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-195-835-258

Query Match 86.2%; Score 50; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.9e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 1 CMTWNQMNL 9

Search completed: March 17, 2007, 07:44:55
 Job time : 405 secs

Sugiyama 10527692 UniProt search

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2007, 07:29:19 ; Search time 365 Seconds
(without alignments)
26.436 Million cell updates/sec

Title: US-10-527-692-3
Perfect score: 58
Sequence: 1 CYTWNQMNL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_8.4:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	50	86.2	239	1 WT1_SMIMA	P49953 sminthopsis
2	50	86.2	249	2 Q6PI38_HUMAN	Q6pi38 homo sapien
3	50	86.2	251	2 Q866X3_SHEEP	Q866x3 ovis aries
4	50	86.2	288	1 WT1_ALLMI	P50902 alligator m
5	50	86.2	302	2 Q4VXV4_HUMAN	Q4vxv4 homo sapien
6	50	86.2	305	2 Q199A7_MOUSE	Q199a7 mus musculu
7	50	86.2	392	2 Q91030_CHICK	Q91030 gallus gall
8	50	86.2	407	2 P79958_XENLA	P79958 xenopus lae
9	50	86.2	409	2 Q91657_XENLA	Q91657 xenopus lae
10	50	86.2	414	2 Q9I8A1_CHICK	Q9i8a1 gallus gall
11	50	86.2	417	2 Q9I8A0_CHICK	Q9i8a0 gallus gall
12	50	86.2	426	2 Q9W611_CYNPY	Q9w611 cynops pyrr
13	50	86.2	429	2 Q4VXV5_HUMAN	Q4vxv5 homo sapien
14	50	86.2	432	2 Q4VXV6_HUMAN	Q4vxv6 homo sapien
15	50	86.2	448	1 WT1_RAT	P49952 rattus norv
16	50	86.2	449	1 WT1_HUMAN	P19544 homo sapien
17	50	86.2	449	1 WT1_MOUSE	P22561 mus musculu
18	50	86.2	449	1 WT1_PIG	O62651 sus scrofa
19	46	79.3	416	2 O93433_FUGRU	O93433 fugu rubrip
20	46	79.3	434	2 Q4S0X7_TETNG	Q4s0x7 tetraodon n
21	44	75.9	461	2 Q4HZI2_GIBZE	Q4hzi2 gibberella
22	41	70.7	337	2 Q1WVR3_LACS1	Q1wvr3 lactobacill
23	41	70.7	565	2 Q8EF68_SHEON	Q8ef68 shewanella
24	40	69.0	131	2 Q2UP59_ASPOR	Q2up59 aspergillus
25	40	69.0	252	2 Q172F1_AEDAE	Q172f1 aedes aegyp
26	40	69.0	563	2 Q59QJ0_CANAL	Q59qj0 candida alb
27	40	69.0	890	2 Q24AT3_TETTH	Q24at3 tetrahymena

28	40	69.0	921	2	Q9FN05_ARATH	Q9fn05 arabidopsis
29	40	69.0	1124	2	Q748I0_GEOSL	Q748i0 geobacter s
30	40	69.0	1126	2	Q73ME8_TREDE	Q73me8 treponema d
31	40	69.0	1140	2	Q73L45_TREDE	Q73l45 treponema d
32	40	69.0	1488	2	Q73L43_TREDE	Q73l43 treponema d
33	40	69.0	1561	2	Q4N259_THEPA	Q4n259 theileria p
34	40	69.0	3320	2	Q73MF0_TREDE	Q73mf0 treponema d
35	39.5	68.1	597	2	Q2FA86_9BETA	Q2fa86 cercopithec
36	39.5	68.1	597	2	Q7TFD2_RHCM6	Q7tfd2 rhesus cyto
37	39	67.2	200	2	Q54UC5_DICDI	Q54uc5 dictyosteli
38	39	67.2	244	2	Q8CJR3_STRCO	Q8cjr3 streptomyce
39	39	67.2	245	2	Q81X89_BACAN	Q81x89 bacillus an
40	39	67.2	407	2	Q98383_9PARA	Q98383 measles vir
41	39	67.2	425	2	Q5CIC1_CRYHO	Q5cic1 cryptospori
42	39	67.2	512	2	Q5NDL8_CIOIN	Q5ndl8 ciona intes
43	39	67.2	525	2	Q6GF00_STAAR	Q6gf00 staphylococ
44	39	67.2	525	2	Q2YUI0_STAAB	Q2yui0 staphylococ
45	39	67.2	527	2	Q9ZAH8_STAAU	Q9zah8 staphylococ

ALIGNMENTS

RESULT 1

WT1_SMIMA

ID WT1_SMIMA STANDARD; PRT; 239 AA.

AC P49953;

DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-1996, sequence version 1.

DT 30-MAY-2006, entry version 37.

DE Wilms' tumor protein (Fragment).

GN Name=WT1;

OS Sminthopsis macroura (Stripe-faced dunnart).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Dasyuromorphia; Dasyuridae; Sminthopsis.

OX NCBI_TaxID=9302;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).

RC TISSUE=Testis;

RX MEDLINE=96068905; PubMed=7478606;

RA Kent J., Coriat A.M., Sharpe P.T., Hastie N.D., van Heyningen V.;

RT "The evolution of WT1 sequence and expression pattern in the

RT vertebrates.";

RL Oncogene 11:1781-1792(1995).

CC -!- FUNCTION: Potential role in transcriptional regulation. Recognizes

CC and binds to the DNA sequence 5'-CGCCCCGC-3' (By similarity).

CC -!- SUBCELLULAR LOCATION: Nucleus.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=P49953-1; Sequence=Displayed;

CC Name=2;

CC IsoId=P49953-2; Sequence=VSP_006875;

CC Note=No experimental confirmation available;

CC -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein

CC family.

CC -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.

CC -----

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CC -----

DR EMBL; X85732; CAA59737.1; -; mRNA.

DR HSSP; P08046; 1AAY.

DR InterPro; IPR000976; Wilms_tumour.

DR InterPro; IPR007087; Znf_C2H2.

DR InterPro; IPR007086; Znf_C2H2_sub.

DR Pfam; PF02165; WT1; 1.

DR Pfam; PF00096; zf-C2H2; 4.

DR PRINTS; PRO0048; ZINCFINGER.

DR ProDom; PD000003; Znf_C2H2; 2.

DR SMART; SM00355; Znf_C2H2; 4.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
KW Metal-binding; Nuclear protein; Repeat; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
FT CHAIN <1 239 Wilms' tumor protein.
FT /FTid=PRO_0000047136.
FT ZN_FING 113 137 C2H2-type 1.
FT ZN_FING 143 167 C2H2-type 2.
FT ZN_FING 173 195 C2H2-type 3.
FT ZN_FING 204 228 C2H2-type 4.
FT VAR_SEQ 198 200 Missing (in isoform 2).
FT /FTid=VSP_006875.
FT NON_TER 1 1
SQ SEQUENCE 239 AA; 27793 MW; 6707678A7259A624 CRC64;

Query Match 86.2%; Score 50; DB 1; Length 239;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTNQMNL 9
| | | | |
Db 42 CMTWNQMNL 50

RESULT 2
Q6PI38_HUMAN
ID Q6PI38_HUMAN PRELIMINARY; PRT; 249 AA.
AC Q6PI38;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 30-MAY-2006, entry version 13.
DE WT1 protein.
GN Name=WT1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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```

CC -----
DR EMBL; BC046461; AAH46461.1; -; mRNA.
DR Ensembl; ENSG00000184937; Homo sapiens.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms_tumour.
DR Pfam; PF02165; WT1; 1.
DR PRINTS; PRO0049; WILMSTUMOUR.
SQ SEQUENCE 249 AA; 25967 MW; 33F53B96A79CBF28 CRC64;

Query Match      86.2%; Score 50; DB 2; Length 249;
Best Local Similarity 88.9%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 CYTWNQMNL 9
        | |||||
Db      235 CMTWNQMNL 243

```

```

RESULT 3
Q866X3_SHEEP
ID Q866X3_SHEEP PRELIMINARY; PRT; 251 AA.
AC Q866X3;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Wilms' tumor 1 protein (Fragment).
GN Name=WT1;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22421136; PubMed=12533429; DOI=10.1095/biolreprod.102.008946;
RA Logan K.A., McNatty K.P., Juengel J.L.;
RT "Expression of wilms' tumor gene and protein localization during
RT ovarian formation and follicular development in sheep.";
RL Biol. Reprod. 68:635-643(2003).
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CC -----
DR EMBL; AY115591; AAM75388.1; -; mRNA.
DR HSSP; Q60980; 1P7A.
DR SMR; Q866X3; 176-251.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms_tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zf-C2H2; 3.
DR PRINTS; PRO0048; ZINCFINGER.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
FT NON_TER 1 1
FT NON_TER 251 251
SQ SEQUENCE 251 AA; 28536 MW; 0112FEB2153CE431 CRC64;

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Query Match      86.2%; Score 50; DB 2; Length 251;
Best Local Similarity 88.9%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 CYTWNQMNL 9
 | | | | |
 Db 61 CMTWNQMNL 69

RESULT 4

WT1_ALLMI
 ID WT1_ALLMI STANDARD; PRT; 288 AA.
 AC P50902;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1996, sequence version 1.
 DT 30-MAY-2006, entry version 37.
 DE Wilms' tumor protein (Fragment).
 GN Name=WT1;
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
 RX MEDLINE=96068905; PubMed=7478606;
 RA Kent J., Coriat A.M., Sharpe P.T., Hastie N.D., van Heyningen V.;
 RT "The evolution of WT1 sequence and expression pattern in the
 RT vertebrates."
 RL Oncogene 11:1781-1792(1995).
 CC -!- FUNCTION: Potential role in transcriptional regulation. Recognizes
 CC and binds to the DNA sequence 5'-CGCCCCCGC-3'.
 CC -!- SUBCELLULAR LOCATION: Nucleus.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P50902-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P50902-2; Sequence=VSP_006874;
 CC Note=No experimental confirmation available;
 CC -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
 CC family.
 CC -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
 CC -----
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 CC -----
 DR EMBL; X85730; CAA59735.1; -; mRNA.
 DR HSSP; P08046; 1AAY.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4..
 DR PRINTS; PR00048; ZINCFINGER.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Alternative splicing; DNA-binding; Metal-binding; Nuclear protein;
 KW Repeat; Transcription; Transcription regulation; Zinc; Zinc-finger.
 FT CHAIN <1 288 Wilms' tumor protein.
 FT /FTId=PRO_0000047135.
 FT ZN_FING 162 186 C2H2-type 1.
 FT ZN_FING 192 216 C2H2-type 2.
 FT ZN_FING 222 244 C2H2-type 3.
 FT ZN_FING 253 277 C2H2-type 4.
 FT VAR_SEQ 245 247 Missing (in isoform 2).
 FT /FTId=VSP_006874.
 FT NON_TER 1 1
 SQ SEQUENCE 288 AA; 33111 MW; 33E26F7DBE7BFDDE CRC64;

Query Match 86.2%; Score 50; DB 1; Length 288;
 Best Local Similarity 88.9%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 89 CMTWNQMNL 97

RESULT 5

Q4VXV4_HUMAN

ID Q4VXV4_HUMAN PRELIMINARY; PRT; 302 AA.
AC Q4VXV4;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 02-MAY-2006, entry version 8.
DE Wilms tumor 1.
GN Name=WT1; ORFNames=AL049692.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Frankland J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AL049692; CAI95760.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms_tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00048; ZINCFINGER.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 302 AA; 34447 MW; 715B121077C0991D CRC64;

Query Match 86.2%; Score 50; DB 2; Length 302;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 91 CMTWNQMNL 99

RESULT 6

Q199A7_MOUSE

ID Q199A7_MOUSE PRELIMINARY; PRT; 305 AA.
AC Q199A7;
DT 11-JUL-2006, integrated into UniProtKB/TrEMBL.
DT 11-JUL-2006, sequence version 1.
DT 11-JUL-2006, entry version 1.
DE Truncated Wilms' tumor protein.
GN Name=Wt1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL;
RA Hossain A., Nixon M., Kuo M.T., Saunders G.F.;
RT "N-terminally Truncated WT1 Protein with Oncogenic Properties
RT Overexpressed in Leukemia.";
RL Submitted (MAY-2006) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; DQ537939; ABF93406.1; -; mRNA.
SQ SEQUENCE 305 AA; 34756 MW; 3EE51D0C7ED621A5 CRC64;

Query Match 86.2%; Score 50; DB 2; Length 305;
Best Local Similarity 88.9%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | |
Db 91 CMTWNQMNL 99

RESULT 7

Q91030_CHICK
ID Q91030_CHICK PRELIMINARY; PRT; 392 AA.
AC Q91030;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Chick Wilm's tumour protein (Fragment).
GN Name=CWT1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole embryo;
RX MEDLINE=96068905; PubMed=7478606;
RA Kent J., Coriat A.M., Sharpe P.T., Hastie N.D., van Heyningen V.;
RT "The evolution of WT1 sequence and expression pattern in the
RT vertebrates.";
RL Oncogene 11:1781-1792(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole embryo;
RA Kent G.R.L.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; X85731; CAA59736.1; -; mRNA.
DR HSSP; Q60980; 1P7A.
DR SMR; Q91030; 318-384.
DR Ensembl; ENSGALG00000012115; Gallus gallus.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms_tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zf-C2H2; 3.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.

FT NON_TER 392 392
SQ SEQUENCE 392 AA; 43869 MW; 761F01D350E4EDBF CRC64;

Query Match 86.2%; Score 50; DB 2; Length 392;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9'
| | | | | | | |
Db 218 CMTWNQMNL 226

RESULT 8

P79958_XENLA

ID P79958_XENLA PRELIMINARY; PRT; 407 AA.

AC P79958;

DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.

DT 07-FEB-2006, entry version 36.

DE WT1 protein.

GN Name=WT1;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Testis;

RX MEDLINE=97074667; PubMed=8917094; DOI=10.1016/0378-1119(96)00143-6;

RA Semba K., Saito-Ueno R., Takayama G., Kondo M.;

RT "cdna clonig and its pronephros-specific expression of the Wilms'

RT tumor suppressor gene, WT1, from Xenopus laevis.";

RL Gene 175:167-172(1996).

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CC

DR EMBL; D82051; BAA11522.1; -; mRNA.

DR PIR; JC5046; JC5046.

DR HSSP; P08046; 1P47.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR000976; Wilms_tumour.

DR InterPro; IPR007087; Znf_C2H2.

DR Pfam; PF02165; WT1; 1.

DR Pfam; PF00096; zf-C2H2; 4.

DR PRINTS; PRO0049; WILMSTUMOUR.

DR ProDom; PD000003; Znf_C2H2; 2.

DR SMART; SM00355; ZNF_C2H2; 4.

DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.

DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 407 AA; 45983 MW; E2554C658005870C CRC64;

Query Match 86.2%; Score 50; DB 2; Length 407;
Best Local Similarity 88.9%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
| | | | | | | |
Db 212 CMTWNQMNL 220

RESULT 9

Q91657_XENLA

ID Q91657_XENLA PRELIMINARY; PRT; 409 AA.

AC Q91657;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE WT1.
 GN Name=WT1;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96363858; PubMed=8725280;
 RX DOI=10.1002/(SICI)1097-0177(199606)206:2<131::AID-AJA2>3.3.CO;2-I;
 RA Carroll T.J., Vize P.D.;
 RT "Wilms' tumor suppressor gene is involved in the development of
 RT disparate kidney forms: evidence from expression in the Xenopus
 RT pronephros.";
 RL Dev. Dyn. 206:131-138(1996).
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 CC -----
 DR EMBL; U42011; AAB53152.1; -; mRNA.
 DR HSSP; P08046; 1P47.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 409 AA; 46186 MW; 2217FC04612CDE10 CRC64;

 Query Match 86.2%; Score 50; DB 2; Length 409;
 Best Local Similarity 88.9%; Pred. No. 3.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 CYTWNQMNL 9
 | |||||
 Db 214 CMTWNQMNL 222

RESULT 10
 Q9I8A1_CHICK
 ID Q9I8A1_CHICK PRELIMINARY; PRT; 414 AA.
 AC Q9I8A1;
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2000, sequence version 1.
 DT 02-MAY-2006, entry version 29.
 DE WT1(-KTS) protein.
 GN Name=WT1(-KTS);
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RA Kudo T.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AB033633; BAA94793.1; -; mRNA.
 DR HSSP; P08046; 1P47.
 DR Ensembl; ENSGALG00000012115; Gallus gallus.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PRO0049; WILMSTUMOUR.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
 SQ SEQUENCE 414 AA; 46641 MW; 17EB22F8B428A2EF CRC64;

 Query Match 86.2%; Score 50; DB 2; Length 414;
 Best Local Similarity 88.9%; Pred. No. 3.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 218 CMTWNQMNL 226

RESULT 11
 Q9I8A0 CHICK
 ID Q9I8A0_CHICK PRELIMINARY; PRT; 417 AA.
 AC Q9I8A0;
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2000, sequence version 1.
 DT 02-MAY-2006, entry version 30.
 DE WT1(+KTS) protein.
 GN Name=WT1(+KTS);
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RA Kudo T.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AB033634; BAA94794.1; -; mRNA.
 DR UniGene; Gga.4294; -.
 DR HSSP; P08046; 1P47.
 DR Ensembl; ENSGALG00000012115; Gallus gallus.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.

DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
 SQ SEQUENCE 417 AA; 46958 MW; 47BBF7F6448E7F6C CRC64;

Query Match 86.2%; Score 50; DB 2; Length 417;
 Best Local Similarity 88.9%; Pred. No. 3.3;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 218 CMTWNQMNL 226

RESULT 12

Q9W611_CYNPY

ID Q9W611_CYNPY PRELIMINARY; PRT; 426 AA.
 AC Q9W611;
 DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1999, sequence version 1.
 DT 02-MAY-2006, entry version 32.
 DE WT1.
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=99081568; PubMed=9865970;
 RX DOI=10.1046/j.1440-169X.1998.t01-4-00004.x;
 RA Nakayama Y., Yamamoto T., Matsuda Y., Abe S.-I.;
 RT "Cloning of cDNA for newt WT1 and the differential expression during
 RT spermatogenesis of the Japanese newt, Cynops pyrrhogaster.";
 RL Dev. Growth Differ. 40:599-608(1998).
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 CC -----
 DR EMBL; AB013888; BAA76399.1; -, mRNA.
 DR HSSP; P08046; 1P47.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
 SQ SEQUENCE 426 AA; 47591 MW; 46A0B158A9F79C6C CRC64;

Query Match 86.2%; Score 50; DB 2; Length 426;
 Best Local Similarity 88.9%; Pred. No. 3.4;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
 | |||||
 Db 225 CMTWNQMNL 233

RESULT 13
Q4VXV5_HUMAN
ID Q4VXV5_HUMAN PRELIMINARY; PRT; 429 AA.
AC Q4VXV5;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 02-MAY-2006, entry version 10.
DE Wilms tumor 1.
GN Name=WT1; ORFNames=AL049692.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Frankland J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; AL049692; CAI95759.1; -; Genomic_DNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms_tumour.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF02165; WT1; 1.
DR Pfam; PF00096; zf-C2H2; 4.
DR PRINTS; PR00049; WILMSTUMOUR.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 429 AA; 47195 MW; C2F9912E0A4DA3DB CRC64;

Query Match 86.2%; Score 50; DB 2; Length 429;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTNQMNL 9
| | | | | | |
Db 235 CMTWNQMNL 243

RESULT 14
Q4VXV6_HUMAN
ID Q4VXV6_HUMAN PRELIMINARY; PRT; 432 AA.
AC Q4VXV6;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 02-MAY-2006, entry version 10.
DE Wilms tumor 1.
GN Name=WT1; ORFNames=AL049692.1-003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Frankland J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC -----
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 CC -----
 DR EMBL; AL049692; CAI95758.1; -; Genomic_DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000976; Wilms_tumour.
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF02165; WT1; 1.
 DR Pfam; PF00096; zf-C2H2; 4.
 DR PRINTS; PR00049; WILMSTUMOUR.
 DR ProDom; PD000003; Znf_C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
 KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
 SQ SEQUENCE 432 AA; 47511 MW; 1ACA6CE3563DA9D2 CRC64;

Query Match 86.2%; Score 50; DB 2; Length 432;
 Best Local Similarity 88.9%; Pred. No. 3.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYTWNQMNL 9
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 Db 235 CMTWNQMNL 243

RESULT 15

WT1_RAT
 ID WT1_RAT STANDARD; PRT; 448 AA.
 AC P49952;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1996, sequence version 1.
 DT 30-MAY-2006, entry version 44..
 DE Wilms' tumor protein homolog.
 GN Name=Wt1; Synonyms=Wt-1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1; 2; 3 AND 4).
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=93046155; PubMed=1330293;
 RA Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;
 RT "Molecular cloning of rat Wilms' tumor complementary DNA and a study
 RT of messenger RNA expression in the urogenital system and the brain.";
 RL Cancer Res. 52:6407-6412(1992).
 CC -!- FUNCTION: Potential role in transcriptional regulation. Recognizes
 CC and binds to the DNA sequence 5'-CGCCCCCGC-3'.
 CC -!- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
 CC Interacts with WTAP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nucleus.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=P49952-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P49952-2; Sequence=VSP_006872, VSP_006873;
 CC Name=3;
 CC IsoId=P49952-3; Sequence=VSP_006872;
 CC Name=4;
 CC IsoId=P49952-4; Sequence=VSP_006873;
 CC -!- TISSUE SPECIFICITY: Kidney.
 CC -!- DEVELOPMENTAL STAGE: Expressed during kidney development.
 CC -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
 CC family.


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CC      -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; X69716; CAA49373.1; -; mRNA.
DR      UniGene; Rn.92531; -.
DR      HSSP; P08046; 1F2I.
DR      TRANSFAC; T02352; -.
DR      Ensembl; ENSRNOG00000013074; Rattus norvegicus.
DR      RGD; 3974; Wt1.
DR      InterPro; IPR000976; Wilms_tumour.
DR      InterPro; IPR007087; Znf_C2H2.
DR      Pfam; PF02165; WT1; 1.
DR      Pfam; PF00096; zf-C2H2; 4.
DR      PRINTS; PR00049; WILMSTUMOUR.
DR      ProDom; PD000003; Znf_C2H2; 2.
DR      SMART; SM00355; Znf_C2H2; 4.
DR      PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR      PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW      Alternative splicing; Anti-oncogene; Cell cycle; DNA-binding;
KW      Metal-binding; Nuclear protein; Repeat; Transcription;
KW      Transcription regulation; Zinc; Zinc-finger.
FT      CHAIN          1      448      Wilms' tumor protein homolog.
FT                                     /FTId=PRO_0000047134.
FT      ZN_FING        322      346      C2H2-type 1.
FT      ZN_FING        352      376      C2H2-type 2.
FT      ZN_FING        382      404      C2H2-type 3.
FT      ZN_FING        413      437      C2H2-type 4.
FT      COMPBIAS        27       82      Pro-rich.
FT      VAR_SEQ         249      265      Missing (in isoform 2 and isoform 3).
FT                                     /FTId=VSP_006872.
FT      VAR_SEQ         407      409      Missing (in isoform 2 and isoform 4).
FT                                     /FTId=VSP_006873.
SQ      SEQUENCE      448 AA;  49193 MW;  329AC9AC1FF73F76 CRC64;

      Query Match          86.2%;  Score 50;  DB 1;  Length 448;
      Best Local Similarity 88.9%;  Pred. No. 3.6;
      Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

Qy          1 CYTWNQMNL 9
            | |||||
Db          234 CMTWNQMNL 242

Search completed: March 17, 2007, 07:35:26
Job time : 367 secs

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